

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	629	25.8	457	1	W84137	A delta-6 desatura
2	629	25.8	457	1	W95504	Mortierella alpina
3	620	25.5	457	1	W85121	A delta-6 desatura
4	535	22.8	355	1	W84139	Desaturase enzyme
5	412	16.9	746	1	W84156	Human desaturase e
6	412	16.9	746	1	W85135	A desaturase enzym
7	412	16.9	753	1	W95514	Amino acid sequenc
8	409.5	16.8	448	1	R93455	Borage delta-6-des
9	409.5	16.8	448	1	W67471	Borage delta-6 des
10	409.5	16.8	448	1	W98130	Borage delta-6 des
11	407.5	16.7	446	1	W85122	A delta-6 desatura
12	312.5	12.8	608	1	W84155	Human desaturase e
13	312.5	12.8	608	1	W85134	A desaturase enzym
14	312.5	12.8	615	1	W95513	Amino acid sequenc
15	284.5	11.7	87	1	W84144	Desaturase enzyme
16	259.5	10.7	252	1	W84141	Desaturase enzyme
17	250.5	10.3	555	1	W84154	Human desaturase e
18	250.5	10.3	555	1	W85133	A desaturase enzym
19	250.5	10.3	562	1	W95512	Amino acid sequenc
20	246.5	10.1	306	1	W84153	Human desaturase e
21	246.5	10.1	306	1	W85132	A desaturase enzym
22	245.1	10.1	306	1	W95511	Amino acid sequenc
23	230.5	9.5	446	1	W85119	A delta-5 desatura
24	230.5	9.5	446	1	W95506	Mortierella alpina
25	213	8.7	359	1	R34102	Bacterial delta-6-
26	211	8.7	359	1	R98456	Synechocystis delt
27	211	8.7	359	1	W85123	A delta-6 desatura
28	211	8.7	365	1	W85124	A delta-6 desatura
29	198	8.1	143	1	W84145	Desaturase enzyme
30	181.5	7.5	211	1	W84151	Human desaturase e
31	181.5	7.5	211	1	W95130	A desaturase enzym
32	181.5	7.5	218	1	W95509	Amino acid sequenc
33	179	6.9	131	1	W84143	Desaturase enzyme
34	168.5	6.4	382	1	W83353	Vernonia galamenen
35	165.5	6.8	379	1	R33699	Sequence of soybea
36	147.5	6.1	384	1	W24997	Microsomal delta-1
37	147.5	6.1	384	1	W94055	Amino acid sequenc
38	147.5	6.1	384	1	W94049	Amino acid sequenc
39	146.5	6.0	384	1	W86155	Protein sequence

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QY 71 PPOAAVNEAQEDFRKLEELIATGMD--ASPLWYSYKISTTLGLGVL-GYFLAVQYQMY 127
Db 83 -RDPQVSEVRDYRMAAEFRKLGLENKGVHTLTYLAFAVAMFLGVLGYLACTSVFAH 141
QY 128 FIGAVLLGMHYQOQWLSHSDICHQTFKRNMMNLVGLVFGNGLQGFVSVTCWKRHNAAH 187
Db 142 QIAAALLGLWIOSAYIGHDSGHVIMSNKSYNRFQALLSNCNLTGISIAWKKTHNAH 201
QY 188 SATNVQGHDDIDNLPPLANSE-----DDVTRASPISRKLIQFOQY-YFLVICI 235
Db 202 LACNSLDYDPLQHIPVFAVSTKFSLSRFDYRKLTDFDVARFLVSYQHTYYPVNCF 261
QY 236 --LLRFTWCFCVLTVRSKDRDNQFYRSQYKKEAIGLALHWTALKALFFMPSILTS 293
Db 262 GRNLFLOTLLFLLSKREVDRALNF-----AGILVFWT-----PLLVSC 301
QY 294 L-----VFFVSELVGGFGIAIVVF-MNHYPLE-KIGDPVWDGHSFGVSGIHTMTNRRG 345
Db 302 LPNWERFFVFTSFTALQHIQFTLNHFAADVVGPTT--GSDWFEKQAAGRIDISCR 359
QY 346 IITDWFEGGLNYQIEHHLWTLPRHNTAVSYQVEQLCQKHNLPYRNPPLPHEGLVILLRY 405
Db 360 SYMD-PFGGLQFOLEHHLFPLRCHPRKVPFVVOELCKRKHLPYRSMSWFEANVLINT 418
QY 406 LAVFARMA 413
Db 419 LKTAANYQA 426

RESULT 11
QY500 PRELIMINARY; PRT; 445 AA.
AC QY500;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DE DELTA-6 FATTY ACID DESATURASE.
GN CYB5PP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA LI W., METZGER M.L., CASKEY C.T., PETRUKHIN K.;
RT "Human retina-specific delta 6 fatty acid desaturase.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF134404; AAD31282.1; -.
SQ SEQUENCE 445 AA; 51145 MW; 7D975F81 CRC32;

Query Match 19.4%; Score 443.5; DB 4; Length 445;
Best Local Similarity 29.8%; Pred. No. 3.7e-33;
Matches 123; Conservative 61; Mismatches 160; Indels 69; Gaps 14;

QY 11 LQLEOTYDVSAMVNFPHPGAEIENYQGRDATDAFVMVH----FOAEKDKLRMPKINP 66
Db 39 LVIERVYDISWAQRHPPGSRUGLIGHGAEDATDAFPHQDUNFVRKFLQPLLIGELAP 98
QY 67 SFELPPQAAVNEAQ--EDFRKLEELIATGMDASPLWYSYKISTTLGLGVLGYFLMVOY 124
Db 99 --EESQDGLPNAQLVEDFRALHQAEDMKLFDASTFFFAFLGLHILAMEVLAWLL---- 153
QY 125 QMYFIG-----AVLLGMHYQOQWLSHSDICHQTFKRNMMNLVGLVFGNGLQGF 175
Db 153 -IYLLGGVWPVSAALAFILASQAQSWCLQHDLGHASIFKSWNNHVAQKFMVQGLKGS 211
QY 176 VTCWKRHNAAHSATNVQGHDDIDNLPPLANSEDDVTRASPISRKLIQFOQ--YFLV- 233
Db 212 AHWNFRHFQHAKNPFIHKDDPVTVAFLGESSVEYGGKKRRYLPYNQOHLFFELG 271
QY 233 --ICILRFIWCFCVLTVRSKDRDNQFYRSQYKKEAIGLALHWTALKALFFMPSILTS 283

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Db 272 PPLTLTVNF-----EVENLAY-----MLVCMQWADLLWAASTYARFFL 309
QY 284 FFMPSI-LTSLVFFVS-ELVGGFGIAIVVFMNMHYPLEKIGDPVWDGH-----GFSVQGIH 337
Db 310 SYLPFYGPVGLVFFFAVRVLESHWFVWITQMNHPKE-----IGHEKRDWVSOLA 362
QY 338 ETNNIRGIITDFFFGGLNQIEHHLWTLPRHNTAVSYQVEQLCQKHNLPY 390
Db 363 ATCNVEPSLTNFWFSGHLNFQIEHHLFPRMHRNYSRVAPLVKSLCAKHGLSY 415

RESULT 12
QY4353 PRELIMINARY; PRT; 448 AA.
AC QY4353;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DE DELTA 6 DESATURASE.
OS Borago officinalis (Bourrache).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids I; unclassified euasterids I;
OC Boraginaceae; Borago.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97268723.
RA SAYANOVA O., SMITH M.A., LAPINSKAS P.A., STOBART K., DOBSON G.;
RA CHRISTIE W.W., SHEWRY P.R., NAPIER J.A.;
RT "Expression of a borago desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
DR EMBL; U79010; AAC49700.1; -.
DR MENDEL; 15845; Borof;2419;15845.
DR PFAM; PF00173; hemeL1; 1.
SQ SEQUENCE 448 AA; 51634 MW; 539A4EDA CRC32;

Query Match 19.2%; Score 437.5; DB 10; Length 448;
Best Local Similarity 29.6%; Pred. No. 1.4e-32;
Matches 120; Conservative 65; Mismatches 171; Indels 49; Gaps 12;

QY 11 LQLEOTYDVSAMVNFPHPGAEIENYQGRDATDAFVMVHFOEAFDKLRMPKINPSFEL 70
Db 25 ISIQKAYDVSQWYKDHPPGSGFPLKSLAQEVTDAEVAFHASTW---KNLDFFTGYL 81
QY 71 PPOAAVNEAQEDFRKLEELIATGMDA-----SPLWYSYKISTTLGLGVLGYFLMVOY 124
Db 82 -KDYSVSEVKDYRKLVTFEFSKMGULYDKKGHINFATLCE---IAMLFAMSVYGVLFCEGV 137
QY 125 QMYFIGAVLLGMHYQOQWLSHSDICHQTFKRNMMNLVGLVFGNGLQGFVSVTCWKRHN 184
Db 138 LVHLFSGCLMGLWISQWIGHDAGHYMVVSDSRNKKFNGIFAANCLSGISIGWKKNNH 197
QY 185 AHSATNVQGHDDIDNLPPLANS-----EDDVTRASPISRKLIQFOQYFLV 232
Db 198 AHHAACNSLEYDPLQYIPFLVVSFKFGSLASHFEYKRLTFDS-LSREFVSQHWTFYP 256
QY 233 ICILRFIWCFCVLTVRSKDRDNQFYRSQYKKEAIGLALHWTALKALFFMPSILTS 292
Db 257 IWCARLNMYVOSLI---MLLTRNVSYRA-----HELGLCVFSIWPVLVSC 302
QY 293 L-----LVFFVSELVGGFGIAIVVF-MNHYPLE-KIGDPVWDGHSFGVSGIHTMTNRRG 345
Db 303 LPNWERIMFVIASLVTGQVQVQSLNHFSSSVVVGKP--KGNWFEKQDTGTLDISCP 360
QY 346 IITDWFEGGLNQIEHHLWTLPRHNTAVSYQVEQLCQKHNLPY 390
Db 361 PMWDFHFGLOQIEHHLFPPKMPRCNKRKISPYVIELCKKHNLPY 405

RESULT 13

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RC STRAIN-CV. DRAKKAR; TISSUE-RIPENING EMBRYOS;
RX MEDLINE; 99003197.
RA SHERLING P., ZAHRINGER U., HEINZ E.;
RT "A sphingolipid desaturase from higher plants
RT cytochrome b5 fusion protein.";
RL J. Biol. Chem. 273:28590-28596(1998).
DR EMBL; AJ224160; CAA11857.1; -.
DR HSSP; P00173; IAGA.
DR MENDEL; 34704; Brana.2419:34704.
SQ SEQUENCE 449 AA; 51490 MW; F9BB69EE CRC3

Query Match	21.88;	Score 498;	DB 10;	Length 449;
Best Local Similarity	32.08;	Pred. No. 3.2e-38;		
Matches 135; Conservative	72;	Mismatches 177;	Indels 38;	Gaps 13;
QY	11	LQMLEQYDVDSAWNFHPGGAEIETENYQGRDATDAFVMYMHFOEAFDKLKRMPKINPSEL	70	
DB	26	ISIOGKYDVDSHWKSPHGGGAALNLAGQDVTDAFIAYHFGTAW--RPHENLHNGXHV	82	
QY	71	PPQAAVNEAOEDFRKLREELIATGMFAS----PLWYSYKITTIGLGLVGLYFELMVQVQY	127	
DB	83	KDH-HVSDVSRDYRRLAAEFKRGFLDKKHWTLYTLTCVAAMLAAYVYGVVACTSIWAH	141	
QY	128	FIGAVILGMHYQMGWNLSDHCICHQTFKRNRNWNLVGLVFGNGLOGFSVTCWKDRHNAHH	187	
DB	142	LISAVILGLGLWIOAYYGHDSGHYNTSTKPCNKLVQLLNSCINTGTSIAWKKWTHNAHH	201	
QY	188	SATNVQGHDPDIDNLPPLAWSE--DDVTRA-----SPISRKLIQFOQY-YFLVVICI	235	
DB	202	ISCSNLSDHPDLQHPVLAVSNKTFKSMTSREYGRKLTDFDLAREFLISYQHWSEVPINCV	261	
QY	236	--LURFWICFOCVITVRSCLKDRDNOFYRSQYKKEAIGLALHWLTKALPHLEFMMPSILSL	293	
DB	262	GRINLFQITLTLFLFSRRYVDPD-----ALNIAGILVFETWFPPLL-VSFLPNWQERI	311	
QY	294	LVFFVSELVGGFGTAIVVF-MNHVPLEKIGDPVWDGHGFSVQIHEWTNIRRGITTDWFF	352	
DB	312	IFVFLSMAY--TAQHVOFCNLHFAADVYTGP-NGNDWFPEKQTAGTLDISCRSYMDFEF	368	
QY	353	GGLNYQIEHHLWPTLPRHNLTAVSQVBOLCQKHNLPYRNPFLPHEGLVILLRYL---AVF	409	
DB	369	GGIOLEHHLHFLPRLPRCHLGRGVSVOELCKKHNLPYRSLSWEEANYTILTRKAAVO	428	

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DR HSP; P00171; LWDB.  
SR MENDEL; 34619; Arach.; 2419; 34619.  
SQ SEQUENCE 449 AA; 51675 MW; 36C26D4D CRC32;  
  
Query Match      21.4%; Score 488.5; DB 10; Length 449;  
Best Local Similarity 30.5%; Pred. No. 2.5e-37;  
Matches 131; Conservative 67; Mismatches 179; Indels 53; Gaps  
:  
QY 11 LQLMEOTDYDSAVNMFHPGGAETIENYOGRDATAPFMVHFQAEFKLRMPKINPSFEL 70  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 26 IATOGKYVNYSDIKTTHPGGDVTILNLVGODVDTAFAEFGCTAWHLLDH---LFTGYHI 82  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
QY 71 PPQAANVEAODEFRKLREELIATGMFD--ASPLWASYKIITTLGLGVL-GYFLMVOYQM 127  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 83 -RDFQSEVSERDYRMVAEFRLKGLPENKGHVLTLYLAFAAMFLGVLGYVLACTSVFAH 141  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
QY 128 FIGAVLLGHMYQQGWLSHDCHHQTFKKRNWNLVGLVFNGLGQFSVTCWKDRHNNAHH 187  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 142 QIAAAALLGLMIQSAYIGHSDSHYIVMSKNKSYNRFAQLSGNCLTGISIAWWKWTHNAHH 201  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
QY 188 SATNVQHGDPIIDLNPALPWLSE-----DDVTRASPTSRKLIQFOOY-YFLVICI 235  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 202 LACNSLDYDPDLQHVPFAVSTKFSSLSRFYDKRLTDPVARFLVSIOHTTYIPVMCF 261  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
QY 236 --LLREFTWFCQCULTVRSLKDRDNQRYRSQYKKEAGIALHWTKALF-----HLF 284  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 262 GRINFLOTLELLFSKRVPDRALNF-----AGILVFWTFPELLVSLCPNMPPERFF 312  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
QY 285 FMSILTSLVFFVELSNGFGGAIYVFNWHYPLE-KIGDPVWDHGFGSVGOIHETMNIR 343  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 313 F---VFTSFVTVALQH-----IOFTLNHFAADYYVGPPT--GSDFEKOAAGTIDIS 359  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
QY 344 RGIITDWFFGGNLNQTEHHLMPTLPRLNTAVSYQEOLCQKHNLPLYRNPHEGLVILL 403  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 360 CRSYNDFWFFGLOFQLEHHLFPRLPRCLRKVSPVVQELCKKHNLPHYRSMWFVANVLT 419  
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
QY 404 RYLAVAFARMA 413  
   |_____|  
Db 420 NTLKTAAYQA 429  
   |_____|  
  
RESULT 10  
Q9ZtZ9 PRELIMINARY; PRT; 446 AA.  
ID Q9ZtZ9  
DC Q9ZtZ9;  
AT 01-MAY-1999 (TREMBrel. 10, Created)  
DT 01-MAY-1999 (TREMBrel. 10, Last sequence update)  
DT 01-NOV-1999 (TREMBrel. 12, Last annotation update)  
DE FATY ACID DESATURASE/CYTOCROME B5 FUSION PROTEIN.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC euryphylliphytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
OC Arabidopsis.  
CN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=DEVELOPING SILIQUES;  
CA SAYANOVA O., STOBART A.K., SHEWERY P.R., NAPIER J.A.;  
RL Submitted (Apr-1997) to the EMBL/GenBank/DDBJ databases.  
DR ENBL; AF001394; AAD00895.1; .  
DR HSP; P00171; LWDB.  
SR MENDEL; 35700; Arach.; 2419; 35700.  
SQ SEQUENCE 446 AA; 51247 MW; 18C9FF05 CRC32;
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Query Match      19.7%; Score 449; DB 10; Length 446;
Best Local Similarity 29.7%; Pred. No. 1.le-33;
Matches 127; Conservative 68; Mismatches 181; Indels 52; Gaps
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Qy 11 LQLMEQTYDSAVWNPHFGAAEIIENYQGRDADTADFVMMHFQEAFLKRMKPINSFEL 70
.:
Db 26 IAIQGVNYSMDIKTHPGGDVTILNLVGQDVDAFAIHPGTAMHHLDR--LFTGYHI 82

Oy	182	RHNAHSATNVQGHDPDIDNLPLPAWSEDDVTRASPIS--RKLIQFOQQYFFLVICILLRF	2339
Dd	207	QHNYHHAAATNYYGRGDGLDVPEYATVAEHLNNYSODSWYMTLFRHQHVHTFMLPFLRL	266
Oy	240	IWFQCQVLTVRSKLRDNQOFVRSQYKEAIGLAHWTLKALFLFWPSPILLSLLVFFVS	299
Dd	267	SWLQSIIIFWSOMPTHYDYRTAIYEQVGLSLHWAW-SLGOLYFLPNOWSTRIMFFLV	325
Oy	300	ELVGFGGIAIVVFMMNHYPLEKIGDPVMWDHGFSVGQIHETMNIIRRGITDWFFGGNLVQI	359
Dd	326	HLVGGFLLSHVVTFNHYSEVKFALSSNIMSNIYAQLQIMTIRNMPPCGRFDLWLWGGLNQI	385
Oy	360	EHLHWPTLPRLNLTAVSYQEQLCKQHNLPY	390
Dd	386	EHLHFTPMRHLNTVMPLYKEFAAANGLPY	416
 RESULT 2			
Q94044 PRELIMINARY; PRT; 454 AA.			
ID	Q94044		
AC	Q94044;		
DT	01-FEB-1997 (TrEMBLrel. 02, Created)		
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)		
DT	01-JAN-1999 (TrEMBLrel. 09, Last annotation update)		
DE	Tl3F2.1 PROTEIN.		
GN	Tl3F2.1.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;		
OC	Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RA	SWBURNE J.:		
RA	Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.		
RL	[2]		
RX	SEQUENCE FROM N.A.		
RP	MEDLINE: 94150718.		
RA	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,		
RA	BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,		
RA	CRAFTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,		
RA	GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,		
RA	JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,		
RA	LIGHTNING J., LLOYD C., McMURRAY A., MORTIMORE B., O'CALLAGHAN M.,		
RA	PARSONS J., PERCY C., REIKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,		
RA	SMAILDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,		
RA	THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,		
RA	WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;		
RT	*2.2 mb of contiguous nucleotide sequence from chromosome III of C.		
RT	elegans.*		
RL	Nature 368:32-38(1994).		
DR	EMBL: 281122; CAB03352.1; -.		
SQ	SEQUENCE 454 AA: 53160 MW; D7FD13FA CRG32;		

QY	233	ICILLRFIWCFCQCVLT	VRSLKDRDNQFVRSQYKKEAIGLALHWTLKALFLFEMP	SLTS	2923
Db	267	MLPFLRLSMLAQSIIF	SOMPTHYDYDYRTAIEQVGLSHWAW-SLGOLYFLPDW	STR	325
QY	293	LLVFVSVLVCGGGIAI	VFNHNHYPLEKIGDPVWDGHSVSGUQIETHMTNRRGI	ITDWF	3523
Db	326	IMFFLVSLVGGFLLSH	VVFVFNHYSVEKFKALSSNIMSNYACLOIMTTRNRRPGR	FIIDLW	3855
QY	353	GGLNYQIEHHLWPTL	PRHNLTAIVSQYEQLCQKHNLPY	390	
Db	386	GGLNYQIEHHLFPT	PRHNLNTVMPLVKEFAAANGLPY	423	
RESULT	3				
O61388		PRELIMINARY;	PRT;	443	AA.
ID	O61388				
AC	O61388;				
DT	01-AUG-1998	(TReMBLrel. 07, Created)			
DT	01-AUG-1998	(TReMBLrel. 07, Last sequence update)			
DT	01-NOV-1998	(TReMBLrel. 08, Last annotation update)			
DE	DELTA6-FATTY-ACID-DESATURASE.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;				
OC	Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 97268723.				
RA	SAYANOVA O., SMITH M.A., LAPINSKA P., STOBART A.K., DOBSON G.,				
RA	CHRISTIE W., SHEWRY P.R., NAPIER J.A.;				
RT	"Expression of a borage desaturase cDNA containing an N-terminal				
RT	cytochrome B5 domain results in the accumulation of high levels of				
RT	delta6-desaturated fatty acids in transgenic tobacco."				
RL	Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 98149727.				
RA	NAPIER J.A.; HEY S. J., LACEY D.J., SHEWRY P.R.;				
RT	"Identification of a Caenorhabditis elegans Delta6-fatty-acid-				
RT	desaturase by heterologous expression in Saccharomyces cerevisiae."				
RL	Biochem. J. 330:0-0(0).				
DR	EMBL; AF031477; AAC15586.1; -.				
SQ	SEQUENCE 443 AA; 51740 MW; EE44468D CRC32;				

Query Match 27.4%; Score 625; DB 5; Length 454;
Best Local Similarity 36.4%; Pred. No. 5.2e-50;
Matches 145; Conservative 64; Mismatches 151; Indels 38; Gaps 10;

Best Local Similarity 20.7%; Pred. No. 0.0067;
Matches 82; Conservative 65; Mismatches 153; Indels 96; Gaps 25;

QY 29 GAAEIIENYQGRDATDAFVWVHFOEAFDKLRMPKINPSFEL-----PPQAAVNEAQE 81
DB 2 GSLIGSEIYD-----KNSFNEFEF--FD-----PSAPPPERLAEIRNVPKHCHWVXDPLR 50

QY 82 DFRKREELIATGMFASPLWYKISTITGLGV--LGYFLMVQYQMYFVIGAVLLGHYQQ 140
DB 51 SLISVVRDVF-----VATLIGIAHLDSNLF--YPLW---AIOGMFWA 91

QY 141 MGWLSHDICHQHTKRN--WNNLVGLVFGNGL-----OGFSVTCWKDRHNAHHSATNVQGH 195
DB 92 IFVLGHD--CGHGSFSDSLLNNVVGHLHSAILVPYHG-----WRISHKTHH-----QNH 140

QY 196 -DPDIDNLPPLAWSEDDVTRASPISRKLIQFQYFVLVICILLRF--IWCFOCVLTVRSLK 253
DB 141 GNVTDE---SW-----VPMPEKLYNKVGYSTKFLYKIPFPPLAIPMYLMKRSPG 188

QY 254 DRONQF-----YRQYKKEAIGLALHWTALKALHFFMPSI--LTSLLVFFVSELYGGF 305
DB 189 KGSCHENPYSDLQFQPKYVVTSTLCVTYMAALLLYLCTAFGLQMKFYGAPYLIFVM 248

QY 306 GIAVFMNHPYLEKIGDPVMDGHGFSVGOIHETMNRIGIIT---DW-PFGGLNVOIE- 361
DB 249 WLDFVYTLHHGGEK-KLPYRGKEWSY-----LRGLTTVDYDYGLEFNHHDIGT 299

QY 361 ---HHLWPTLPRNLTAVSYQVEQLCOKHNLPRNP 393
DB 300 HVIIHLFPQIPHVHLREATKAAPVGLGKY---YREP 332

RESULT 14
FD3C-SOYBN STANDARD; PRT: 453 AA.

AC P48621;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN PAD7.

OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Glycine.
[1]

RN SEQUENCE FROM N.A.
RP TISSUE=SEED;
RX MEDLINE; 94302147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMANN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL Plant Physiol. 103:467-476(1993).

CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION-BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC

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or send an email to license@isb-sib.ch.

CC EMBL; L22965; AAA61776.1; -
DR PIR; J02339; J02339.
DR PFAM; PF00487; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transit peptide.
FT TRANSIT 1 ?
FT CHAIN 1 ?
FT CHAIN 2 453
FT DOMAIN 171 175
FT DOMAIN 207 211
FT DOMAIN 374 378
FT SEQUENCE 453 AA; 51362 MW; E4314F1B CRC32;

Query Match 5.1%; Score 117; DB 1; Length 453;
Best Local Similarity 20.3%; Pred. No. 0.01;
Matches 92; Conservative 72; Mismatches 150; Indels 140; Gaps 25;

QY 7 ALSPLQIME--QYDVSANVNFHPGAAEIIENYQGRDATDAFVWVHFOEAFDKL----- 59
DB 26 ALSSTSRVEFLDTNKVVAGPKFQPLRCNLERNWGLKVSAPLRVASIEEESQKSYDLTNGT 85

QY 59 -----KMPKINPSFELPP-----QAAVNE---AQEDFKL---REELIATGMFAS 99
DB 86 NGVEHEKLPEDFG--APPPFNLAIRAAIPKHCWKOPWRSYVYVVRVIAVFGLAANA 143

QY 100 -----PLMYSYKISTITGLGVGLVFLMVQYQMYFVIGAVLLGHYQMGWLSHDICH 150
DB 144 AYLNNWLVPLYWRAQ-----GTFWALFV-----LGHD-CG 174

QY 151 HQTFKRN--WNNLVGLVFGNGL-----OGFSVTCWKDRHNAHHSATNVQGHDPIDNLPPL 205
DB 175 HGSFSNNSKLSVVGHLHSSILVPYHG-----WRISHRTHQH---HGAENDESHP 226

QY 206 A-----WSEDVTRASPISRKLIQFQYFVLVICILLRF-----IWCFOCVLTVRSLK--- 254
DB 227 PEKLFSLDTVTR-----MURFTAPFPPLAIPVYLFSSPKQGT 265

QY 254 ---DRONQFVRSQYKKEAIGLALHWT--LKALFHLFFMPSILTSLLVFFVSELYGGFGIA 308
DB 266 SHEDPSDLFPVNERKDVITSTACWAAMLGLLVGLGVGMGPIQLLKLYGVPYVIFVMWLD 325

QY 309 IYVFMNHPYLE-KIGDPVMDGHGFSVGOIHETMNRIGIIT--DWFFGGLN-----YQI 359
DB 326 LVTYLHHGHGDKL--PWYRGKEWSY-----LRGLTTLDYDYGLEFNHHDIGTHV 375

QY 360 EHLWPTLPRNLTAVSYQVEQLCOKHNLPRNP 393
DB 376 IHLFPQIPHVHLREATEAKAPVGLGKY---YREP 406

RESULT 15
FD3C-SPIOL STANDARD; PRT: 447 AA.

ID FD3C-SPIOL
AC P48629;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD6.

OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Caryophyllales; Caryophyllaceae; Chenopodiaceae;
OC Spinacia.
[1]

RN SEQUENCE FROM N.A., AND SEQUENCE OF 66-78.
RC STRAIN=CV. SUBITO; TISSUE=LEAF;
RX MEDLINE; 9503604.
RA SCHMIDT H., DRUSSELHAUS T., BUCK F., HEINZ E.;
RT "Purification and PCR-based cDNA cloning of a plastidial n-6
RT desaturase.";

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RESULT 12
FD32_BRANA STANDARD; PRT; 383 AA.
AC P48624;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (VERSION 2).
GN FAD3.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Brassica.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 93088059.
RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
RA SOMERVILLE C.R.;
RT "Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.";
RL Science 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
CC EMBL; L01418; AAA32994.1; -.
CC PFAM; PF00487; FA_desaturase; 1.
CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
CC Transmembrane.
CC TRANSMEM 53 73 POTENTIAL.
CC TRANSMEM 210 230 POTENTIAL.
CC TRANSMEM 234 254 POTENTIAL.
CC DOMAIN 98 102 HISTIDINE BOX 1.
CC DOMAIN 134 138 HISTIDINE BOX 2.
CC DOMAIN 301 305 HISTIDINE BOX 3.
CC SEQUENCE 383 AA; 43936 MW; F39A978B CRC32;

Query Match
Best Local Similarity 5.3%; Score 120; DB 1; Length 383;
Matches 78; Conservative 66; Mismatches 136; Indels 96; Gaps 21;

QY 52 QEAFDLKMPKINPSFEL-----PPQAAVNEAQEDFRKLREELIATGMFD 97
DB 20 ESGFD-----PSAQPFPKIDIRAAIPKHCWKSPLRMSYVTRDIFAAALAAVAAYFD 74
QY 98 ASPLWYSKISTLTGLGVGLYLMVQYQMYFICAVLLGHMYQGMWLSHDICHHTQFKNR 157
DB 75 SNFLPLVYVAQ---GTLFWAIFV-----LGHD-CGHGFSF- 108
QY 158 NNNNLVGLVFGNLQGFVSFV---CWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTR 214
DB 108 --IPLNSVVGHLHLSFILVPYHGWIRSHRTHQN---HGVENDESQWPL---PEKLYK 159

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QY 215 ASPISRKLIQOQYFLVICILLRFTWCFOCVLTVRSKLDKDNQF---YRSQY-----KKEA 268
DB 160 NLPHSTRMLR---YTVPLPML-----AYPIYLWYRSPGKEGSHFNYPYSSLFAPSERKLI 210
QY 269 IGLALHWT--LKALFLHLEFMPSTLTLVFFVSELVGGFGIAIVVENHYPYLP-EKIGDPV 325
DB 211 ATSTTCSIMLAIVLSFLVDPVTVLKVIYGVPIYIFVMDLDAVTYLHHGHGDEKL--PW 268
QY 326 WDGHGFGVSGIHTMNIIRGIIT---DW-FFGLNLYQIE-----HHLWPTLPRLHNLTAHSV 377
DB 269 YRGKEWSY-----LRGGLTTIDRDYGIFFNNIHHDTGTHVIHLLFPQIPHYHLVDATR 320
QY 378 QVQLCOCKHNLPRNP 393
DB 321 AAKHVLGRY---YREP 333

RESULT 13
FD3E_TOBAC STANDARD; PRT; 379 AA.
AC P48626;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE FAD3.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
OC Nicotiana.
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN-CV. SRI; TISSUE-LEAF;
RX MEDLINE; 95011632.
RA HAMADA T., KODAMA H., NISHIMURA M., IBA K.;
RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";
RL Gene 147:293-294(1994).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
CC EMBL; D26509; BAA05515.1; -.
CC PFAM; PF00487; FA_desaturase; 1.
CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
CC Transmembrane.
CC TRANSMEM 52 72 POTENTIAL.
CC TRANSMEM 213 233 POTENTIAL.
CC TRANSMEM 236 256 POTENTIAL.
CC DOMAIN 97 101 HISTIDINE BOX 1.
CC DOMAIN 133 137 HISTIDINE BOX 2.
CC DOMAIN 300 304 HISTIDINE BOX 3.
CC SEQUENCE 379 AA; 44149 MW; C237E46D CRC32;

Query Match
5.2%; Score 118; DB 1; Length 379;

```

DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE BETA-CAROTENE KETOLASE (EC 1.13.-.-) (BETA-CAROTENE OXYGENASE).
 GN CRTW.
 OS Agrobacterium aurantiacum.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Agrobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96062243.
 RA MISAWA N., SATOMI Y., KONDO K., YOKOYAMA A., KAJIWARA S., SAITO T.,
 RA OHTANI T., MIKI W.;
 RT "Structure and functional analysis of a marine bacterial carotenoid
 RT biosynthesis gene cluster and astaxanthin biosynthetic pathway
 RT proposed at the gene level."
 RL J. Bacteriol. 177:6575-6584(1995).
 CC -/- CATALYTIC ACTIVITY: CONVERTS BETA-CAROTENE TO CANTHAXANTHIN VIA
 CC ECHINENONE.
 CC -/- PATHWAY: CAROTENOID BIOSYNTHESIS. INVOLVED IN ASTAXANTHIN
 CC BIOSYNTHETIC PATHWAY.
 CC -----
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 CC -----
 CC EMBL: D58420; BAA09591.1;
 KW Carotenoid biosynthesis; Oxidoreductase.
 SQ SEQUENCE 242 AA; 27128 MW; AA7C8248 CRC32;

Query Match 5.4%; Score 123.5; DB 1; Length 242;
 Best Local Similarity 23.2%; Pred. NO. 0.0013;
 Matches 64; Conservative 36; Mismatches 87; Indels 89; Gaps 15;
 QY 114 GVLGYFLMWQ-YQMFIGA-----VLLGMHYQQMGWLS-----HDICHQTKFNR-NWN 160
 DB 21 GIIAALHVLHVAHFLDAAHPIAIAFLGLTSLVGLFIHDAHMGSVVPGRPAN 80
 QY 161 NLVGLVFGNGLQFSVTCWKD---RHNAHSATNVQGHDPDIDNLPPLANSEDDVTRASP 217
 DB 81 AAMGQLVLMYLAGFS---WRKMIVKMAHHRHAGTD-DPDPDFHGGVPRV-----127
 QY 218 ISRKLFQFOQYF-----LVICILLRFIWCFCVLTVRSILKDRDNQFYSQYKKEAIGLA 272
 DB 127 ----YARFTGYGWEGLLPV-----IVTVALLIGDRWF-----V 161
 QY 273 LHWTLKALFHLFPFMSILTSLLVFFVSELVGFGFIAIVFMNHYPLEKIGDPVWDHGFS 332
 DB 162 VFNPL-----PSILASIQLF-----VFTWLPHPRGHDAFPDRNAR 198
 QY 333 VGOIHETMIRRIIITDWFEGGLNYQIEHLWTLTP 368
 DB 199 SRSISDPVS-----LLTCFHEGG--YHREHHLHTPTP 228

RESULT 11
 DESA_SYNY3
 ID DESA_SYNY3 STANDARD; PRT; 351 AA.
 AC P20388;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE FATTY ACID DESATURASE (EC 1.14.99.-) (DELTA 12 DESATURASE).
 GN DESA OR SLR1350.
 OS Synecocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90370121.
 RA WADA H., GOMBOS Z., MURATA N.;

RT "Enhancement of chilling tolerance of a cyanobacterium by genetic
 RT manipulation of fatty acid desaturation."
 RL Nature 347:200-203(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUO A., MURAKI A., NAKAZAKI N., NAKUO K.,
 RA OKUMURA S., SHIMO S., TAKEUCHI C., WADA T., WATANABE A.,
 RA YAMADA M., YASUDA M., TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions."
 RL DNA Res. 3:109-136(1996).
 CC -/- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
 CC POSITION OF FATTY ACID BOUND TO MEMBRANE GLYCEROLIPIDS. THIS
 CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
 CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON
 CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.
 CC -/- SIMILARITY: TO PLANTS STEAROYL-ACP DESATURASE.
 CC -----
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 CC -----
 CC EMBL: X53508; CAA37584.1; -;
 DR EMBL: D90912; BAA18169.1; -;
 DR PIR: S11519; S11519.
 DR PROSITE: PS00574; FATTY-ACID-DESATUR_2; 1.
 DR PFAM: PF00487; FA-desaturase; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Membrane.
 FT DOMAIN 90 94 HISTIDINE BOX 1.
 FT DOMAIN 126 130 HISTIDINE BOX 2.
 FT DOMAIN 287 291 HISTIDINE BOX 3.
 SQ SEQUENCE 351 AA; 40495 MW; 9417F79D CRC32;

Query Match 5.3%; Score 120; DB 1; Length 351;
 Best Local Similarity 23.1%; Pred. NO. 0.0041;
 Matches 93; Conservative 38; Mismatches 135; Indels 136; Gaps 23;
 QY 62 PKINPSFELPQAAVNEAQEDFKRLRELIATGMFADSPWYSYKISTTGLGLVGLYFLM 121
 DB 10 PTVTPSNPDRPIADL-KLQDIITLPECEFEK---KASKAWASVLI--TLGAIAGVGLGI 63
 QY 122 VOQMY-----FIGAVLLGMHYQQMGWLSHDICHQTKFNRNW-NLVG-LVFGNGLQ 172
 DB 64 IYLPWYCLPTIWTGTALTGAFV-----VGHD-CGHRSPAKRWVNDLVGHIAFPLIY 117
 QY 173 GFSVTCWKDRNHAHSATNVQGHDPDIDNLPPLANSEDDVT--RASISRKLFQFOQYF 230
 DB 118 PFH--SWRLLDHHLHTN---KIEVDN---AWDPWSVEAFQASPAIVRL-----160
 QY 231 LVICILLRFIWCFCVLTVRSILKDRDNQFYSQYKKEAIGLALHWTALKALFLFMPISIL 290
 DB 160 -----FYR-----AIRGPFWWT-GSIFH-----177
 QY 291 TSLVFFVSELVG-----GFGIAIVFMN--HYPLEKIGDPVWDHGFGSVGQIHETMNI 342
 DB 177 WSLMHFKLSNFAQDRDNKVKLSIAVYVFLFAIAFPAIITGVW-----221
 QY 343 RRGITDWFEGGLNYQ-----IEHLWPTL---PRHNLTAVSQ-----VE 380
 DB 221 --GFVAFWLPWLVYHFWMTFTIVHHTIPEIRFPAADWSAAEAQLNGTVHCDYPRWVE 278
 QY 381 QLCQKHNLPYRNPPLPHEGLVILLRYLAVFARMAEKOPAGKAL 422
 DB 279 VLCHDINV-----HIPHLSVAIPSYNLRLAHLGSLKENWGPFL 316


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Db 79 GPLSR-----GMAI---YVAVQ-----GCILTV-----WVIAHECGHAFSDYQLL 118
QY 160 NNLVGLVFGNGL--QGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASP 217
Db 119 DIIVGLILHSALLVPYFS---WKYSRRHHSNTG-----SLERDEV--FVP 159
QY 218 ISRKLIOFOQYYF-----LVICILLRFTWCQCCLTVRS-----LKD 254
Db 160 KOKSCIKWYSKYLNNPGRVLTAVTLTGWPLYLALNVSGRPYDRFACHYDYPGIYS 219
QY 255 RON-QYRQYKKEALGLAHWTLKALFLHFFMPSILTSLLVFFVSELVCGFGIAIVFEM 313
Db 220 RERLOIYIS---DAGVLAV---VYGLFRMAKAGLAWVYCVYGVPLLVYNGFLVLTFL 272
QY 314 NH-YP-LEKIGDPVMDGHGFSVGOIHETMNRIRGITDWFPGNLNQIEHHLWPTLPRHN 371
Db 273 QHTHPALPHYTSEWD---WLRGAL-ATVDRDYGILNKVFHNITDTHVAHHLFSTMPHYH 328
QY 372 LTAVSYQVEQLCOKHNLPR 391
Db 329 AMEATRAIKPILGEY---YR 345

RESULT 7
FD6E-ARATH STANDARD; PRT; 383 AA.
AC P46313.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (DELTA-12 DESATURASE).
GN FAD2
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94176997.
RA OKULEY J., LIGHTNER J., FELDMANN K.A., YADAV N., LARK E., BROWSE J.;
RT "Arabidopsis FAD2 gene encodes the enzyme that is essential for
RT polyunsaturated lipid synthesis.";
RL Plant Cell 6:147-158(1994).
CC -!- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLED BOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -!- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -!- SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL; L26296; AAA32782.1; -.
CC PFAM; PF00487; FA_desaturase; 2.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
Transmembrane.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 179 199 POTENTIAL.

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FT TRANSMEM 225 245 POTENTIAL.
FT TRANSMEM 232 272 POTENTIAL.
FT DOMAIN 105 109 HISTIDINE BOX 1.
FT DOMAIN 141 145 HISTIDINE BOX 2.
FT DOMAIN 315 319 HISTIDINE BOX 3.
SQ SEQUENCE 383 AA; 44047 MW; 192C3433 CRC32;

Query Match 5.9%; Score 134; DB 1; Length 383;
Best Local Similarity 20.3%; Pred. No. 0.00029;
Matches 74; Conservative 52; Mismatches 135; Indels 104; Gaps 19;

QY 56 DKLRKPKNPSE-----LPPQAAVNEAQEDFRKLREELATGMFDASPLWYSKIS 108
Db 19 DTKRVPCEKPPESVGDLLKKAIPPHCFKRSFYSYLISDIASCF-----YYVA 70
QY 109 TLTGLGLVGLVFMVQYFY-----GAVLLGMHVQOMGWLSDHCHHOTFKNRNW 159
Db 71 T-----NYFSLLPQPLSYLAWPLYWACOGCVLTGI-----WVIAHECGHAFSDYQW 117
QY 160 -NNLVGLVFGNGL--QGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRAS 216
Db 118 LDDTVGLIFHSFLVPYFS---WKYSRRHHSNTG-----SLERDEV--FV 158
QY 217 PISRKLIQFOQYYF-----LVICILLRFT--WCFQCCLTVRS-----LK 253
Db 159 PKOKSAIKWYKYLNNPLGRIMMLTVQVLGWLPLYLAFNVSGRPYDGFACHFPNAPIYN 218
QY 254 DRDN-QYRQYKKEALGLAH---WTLKALFLHFFMPSILTSLLVFFVSELVCGFGI 307
Db 219 DRERLOIYISDAGILAVCGGLYRYAAAGWASMICLYGVPLL-----IVNAFLV 267
QY 308 AIYVFMNHYF-LEKIGDPVMDGHGFSVGOIHETMNRIRGITDWFPGNLNQIEHHLWPT 366
Db 268 LITVLQHTPSLPHYDSSEWD---WLRGAL-ATVDRDYGILNKVFHNITDTHVAHHLFST 323
QY 367 LPRHN 371
Db 324 MPHYN 328

RESULT 8
FD3C-SESIN STANDARD; PRT; 447 AA.
AC P48620;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids I; Lamiales; Pedaliaceae;
OC Sesamum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. 4294; TISSUE=COTYLEDON;
RA SHOUJI K.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLED BOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -!- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -!- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=CV. 651-2-5-7-4;
 SINGH S.P., VAN DER HEIDE T., MCKINNEY S., GREEN A.;
 "Nucleotide sequence of a cDNA from Brassica juncea encoding a
 microsome omega-6 desaturase";
 (In) Plant Gene Register PGR95-107.
 FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 THE SECOND DOUBLED BOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 PHOSPHOLIPIDS (BY SIMILARITY).
 PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
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 or send an email to license@isb-sib.ch).
 EMBL: X91139; CAA62578.1;
 PFAM: PF00487; FA_desaturase; 2.
 Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 Transmembrane
 TRANSMEM 56 76 POTENTIAL.
 TRANSMEM 84 104 POTENTIAL.
 TRANSMEM 117 137 POTENTIAL.
 TRANSMEM 180 200 POTENTIAL.
 TRANSMEM 226 246 POTENTIAL.
 TRANSMEM 253 273 POTENTIAL.
 DOMAIN 105 109 HISTIDINE BOX 1.
 DOMAIN 141 145 HISTIDINE BOX 2.
 DOMAIN 316 320 HISTIDINE BOX 3.
 SEQUENCE 384 AA; 44315 MW; 13BECED8 CRC32;
 Query Match 6.0%; Score 137.5; DB 1; Length 384;
 Best Local Similarity 21.1%; Pred. No. 0.00014;
 Matches 80; Conservative 54; Mismatches 135; Indels 111; Gaps 20;
 QY 56 DKLRMPKINPSF-----ELPQAAVNEAQEDERKLEELTATGMDASPLWYSKIS 108
 DB 19 DTLKRVPCETPTVGCLEKKAIPHCCKRSPRSFYLWDIVASCF-----YYVA 70
 QY 109 TTLGLVGLYFLMVQYQYFI-----GAVLLGMHYQMGWLSHDICHQTEKRNW 159
 DB 71 TT-----YFLLPPLSVVAMPVWACQGVVLTGV-----WVIAHECGHHAFSDYQW 117
 QY 160 -NNLVGLVFGNGL--QGFSVTCWKDRNHAHSATNVQGHG-----DPID-----NL 202
 DB 118 LDDTVGLIFSHFLVLPYFS--WKYSHRRHNSNTGSLDERDEVFPKKSIDIKWYKLYNN 174
 QY 203 P-----PLAWSDDVTRASPISKRLQFQYFLVICILLRIFWCQCVL 247
 DB 175 PLGRIVMLTVQTLGVLFWAFNVSGRYPEG-----FACHF 211
 QY 248 TVRS--LKDRDNQVRSQ-YKKEAIGLALHWTALKALFLFMPFSILTSLLVFSVSLVGG 304
 DB 212 HENAPIYNDRE---RLQIYVSDAGILAVCY---GLYRYAAAGQVAVSYCLGVPLLIYN 264
 QY 305 FGAIIVFVFNH--YP-LEKIGDPVWGHGFSVGQIHTMIRGIIITDWFEGGLNVOIEHH 362
 DB 265 AFLVLITYLQHTPHPLPHYDSSEWD---WLRGAL-ATVDRDYGILNKVFNHNTIDTTHVAHH 320

QY 363 LWPTLPRHNLTAYSYQVEQL 382
 DB 321 LFTMPHYHAMEVTKAIKPI 340
 RESULT 6
 FD62_SOYBN
 ID PD62-SOYBN STANDARD; PRT; 383 AA.
 AC P48631;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2
 DE (EC 1.14.99.-).
 GN PAD2-2.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
 OC Glycine.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EPICOTYL;
 RA MEDLINE; 96151506.
 RA HEPPARD E.P., KINNEY A.J., STECCA K.L., MIAO G.H.;
 "Developmental and growth temperature regulation of two different
 microsomal omega-6 desaturase genes in soybeans.";
 RT Plant Physiol. 110:311-319(1996).
 RL [1]
 CC FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 THE SECOND DOUBLED BOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 PHOSPHOLIPIDS.
 PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
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 EMBL: L43921; AAB00860.1;
 PFAM: PF00487; FA_desaturase; 2.
 Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 Transmembrane.
 TRANSMEM 61 81 POTENTIAL.
 TRANSMEM 85 105 POTENTIAL.
 TRANSMEM 117 137 POTENTIAL.
 TRANSMEM 179 199 POTENTIAL.
 TRANSMEM 225 245 POTENTIAL.
 TRANSMEM 249 269 POTENTIAL.
 DOMAIN 105 109 HISTIDINE BOX 1.
 DOMAIN 141 145 HISTIDINE BOX 2.
 DOMAIN 315 319 HISTIDINE BOX 3.
 SEQUENCE 383 AA; 43967 MW; CAL65721 CRC32;
 Query Match 5.9%; Score 134.5; DB 1; Length 383;
 Best Local Similarity 21.8%; Pred. No. 0.00026;
 Matches 83; Conservative 56; Mismatches 144; Indels 97; Gaps 21;
 QY 56 DKLRMPKINPSFEL-----PQAAVNEAQEDERKLEEL-----IATGMDASP 100
 DB 19 DPLKRVPEKQFSLSQIKKAIPHCCKRSPRSFYLWDIVASCF-----YYVA 78
 QY 101 LWYSKISTTLGLVGLYFLMVQYQYFI-----GAVLLGMHYQMGWLSHDICHQTEKRNW 159

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FT TRANSIT 1 64 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 65 443 OMEGA-6 FATTY ACID DESATURASE.
FT DOMAIN 166 170 HISTIDINE BOX 1.
FT DOMAIN 202 206 HISTIDINE BOX 2.
FT DOMAIN 362 366 HISTIDINE BOX 3.
SQ SEQUENCE 443 AA: 50755 MW; C814102A CRC32;

Query Match 6.4%; Score 145; DB 1; Length 443;
Best Local Similarity 20.5%; Pred. No. 3.9e-05;
Matches 75; Conservative 55; Mismatches 131; Indels 104; Gaps 17;

QY 71 PPOAAVNEAQED-----FRKLREEL-----IATGMFDASP-----LWYSYKISTT 110
DB 71 PPSADNAEDREOLAESYGFQIGQDLPDNTVTKDINDTLTPKEVFEDDVKAMKSVLSVIT 130

QY 111 LGLGVLYFLMVOYQMYFI-----GAVLLGMHYQOMGWSLSDICHHOTFKRNNNNLV 163
DB 131 --SYALGLFMIKAPWYLLPLAWAWTGTAVTGFFV-----IGHDCAKHSKKNKLVEDIV 183

QY 164 GLVFGNGLOGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPISRKLI 223
DB 184 GTLAEPLV-YPEPFRKDRHAKTNMLVHDTANQPVPP---EEFD---SSPVLKRAI 236

QY 224 QF-----QYYFLV-----ICILLRIWCFQCY---LTVRSKLRD 256
DB 237 IFGYGPIRPLWSIAHVNWHNFNKRFPSEVNRVKISLACVAFMAVGWPLII----- 290

QY 257 NOFYRQYKKEAIGLALHWTLLKALFLHFMPSILTSLLVFFVSELVGGFGIAIVFMNHY 316
DB 290 -----YKVGVLGKFWLWPLWGLYHFWMs---TFTMVHHTAP-----HI 325

QY 317 PLEKIDPDVWDGHGFSVQIHTMNRRIITDWFEGGLNYQIEHHLWPTLPRHNLTAVS 376
DB 326 PKPADE--WNA---AAQLNGIVHCDYPSWIELCHDINVHPHISPIPSYNLRAAH 380

QY 377 YOVEQ 381
DB 381 QSIQE 385

RESULT 4
FD61_SOYBN STANDARD; PRT; 387 AA.
AC P48630:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 1
DE (EC 1.14.99.-).
GN FAD2-1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Glycine.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RX MEDLINE; 96151506.
RA HEPPARD E.P., KINNEY A.J., STECCA K.L., MIAO G.H.;
RT "Developmental and growth temperature regulation of two different
RT microsomal omega-6 desaturase genes in soybeans.";
RL Plant Physiol. 110:311-319(1996).
CC -!- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -!- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.

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CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -!- SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L43920; AAB00859.1;
DR PFAM; PF00487; FA_desaturase; 2.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 183 203 POTENTIAL.
FT TRANSMEM 227 247 POTENTIAL.
FT TRANSMEM 251 271 POTENTIAL.
FT DOMAIN 109 113 HISTIDINE BOX 1.
FT DOMAIN 145 149 HISTIDINE BOX 2.
FT DOMAIN 319 323 HISTIDINE BOX 3.
SQ SEQUENCE 387 AA: 44662 MW; 9F61BE96 CRC32;

Query Match 6.1%; Score 140; DB 1; Length 387;
Best Local Similarity 21.3%; Pred. No. 8.9e-05;
Matches 83; Conservative 56; Mismatches 162; Indels 88; Gaps 19;

QY 58 LKRMKPINPSF-----ELPPOAAVNEAQEDFRKLREELIATGMFDASPLWYSYKISTT 110
DB 26 LSRVPNTKPPFTVGQLKKAIPPHCFORSLLTSESYV-----VYDLSFAFIY-IATT 76

QY 111 LGLGVLYFLMVOYQMYFI--GAVLLGMHYQOMGWSLSDICHHOTFKRNN--NLVGLVLF 167
DB 77 YFHLPPQPSLIAWPIYVWLGCLLTGV-----WVIAHECGHAFSKYQWDDVVGTLT 130

QY 168 NGNL--QGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPISRKLIQF 225
DB 131 HSTLLVPYFS---WKISHRRHSHNTG-----SLDRDEVFVPKPS-KYAVWF 172

QY 226 QYY-----FLVICILLRFIMCFQVLTAVRSKLRDNOFYRQYKKEA----- 269
DB 173 SKYLLNPLGRAVSLVLTATIGWPMYLAFNV---SGRPYDSFASHYHPYAPIYSNRERLLI 229

QY 269 --TGLALHWTLLKALFLHFMPSILTSLLVFFVSEL-VGGFGIAIVFMN-HYPLEKIGDP 324
DB 230 YVSDVALFSVTSYLYRVATLKGVLWLLCVYGVPLLVINGFLVITYLQHTFHALPHYDSS 289

QY 325 VWBGHGFSGVQIHTMNRRIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVEQLC- 384
DB 290 EWD---WLKAL-ATMDRDYGLNKVFFHITDTHVAHLEFSTMPHYHAMEATNAIKPILG 345

QY 384 ---QKHNLPYRNPL-----PHEG 398
DB 346 EYQFDDTTPYKALWREARECLYVPEDEG 374

RESULT 5
FD6E_BRAJU STANDARD; PRT; 384 AA.
ID FD6E_BRAJU
AC Q39287;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (DELTA-12 DESATURASE).
OS Brassica juncea (Leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

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Result No.	Score	Query		ID	Description
		Match	Length		
1	239	10.5	359	LLCD_SVNY3	Q08871 synechocyst
2	145.5	6.4	418	FD6C_ARATH	P46312 arabidopsys
3	145	6.4	443	FD6C_BRANA	P48627 brassica na
4	140	6.1	397	FD61_SOYBN	P48630 glycine max
5	137.5	6.0	384	FD6E_BRAJU	Q39287 brassica ju
6	134.5	5.9	383	FD62_SOYBN	P48631 glycine max
7	134	5.9	383	FD6E_ARATH	P46313 arabidopsys
8	127	5.6	440	FD3C_SSSIN	P48620 sesamum ind
9	126.5	5.5	387	FD3E_PHAHU	P32291 phaseolus a
10	123.5	5.4	421	DESA_SVNY3	P54972 agrobacteri
11	120	5.3	351	CRTA_SVNY3	P20388 synechocyst
12	120	5.3	393	FD32_BRANA	P48624 brassica na
13	118	5.2	379	FD3E_TOBAC	P48626 nicotiana t
14	117	5.1	453	FD3C_SOYBN	P48621 glycine max
15	117	5.1	447	FD6C_SPIOL	P48629 spinacia ol
16	116.5	5.1	460	FD3C_RICCO	P48619 ricinus com
17	114	5.0	380	FD3E_SOYBN	P48625 glycine max
18	113.5	5.0	424	FD6C_SOYBN	P48628 glycine max
19	111	4.9	414	CYBR_DROME	P19967 drosophila p
20	110	4.8	351	DESA_SDIPL	Q54794 spirulina p
21	110	4.8	404	FD3C_BRANA	P48618 brassica na
22	109	4.8	591	CYB2_YEAST	P00175 saccharomyc
23	108.5	4.8	435	FD3D_ARATH	P48622 arabidopsys
24	107.5	4.7	446	FD3C_ARATH	P46310 arabidopsys
25	106.5	4.7	573	CYB2_HANAN	P09437 hansenula a
26	105	4.6	386	FD3E_ARATH	P48623 arabidopsys
27	98	4.3	120	CYB5_YEAST	P40312 saccharomyc
28	97	4.2	339	ACOD_HUMAN	O00767 homo sapien
29	95.5	4.2	358	ACOD_RAT	P07308 rattus norv
30	95	4.2	355	ACOI_MOUSE	P13516 mus musculus
31	95	4.2	133	CYB5_BOVIN	P00171 bos taurus
32	95	4.2	133	CYB5_HUMAN	P00167 homo sapien
33	93.5	4.1	134	CYB5_MUSDO	P49096 musca domes
34	93	4.1	377	FD31_BRANA	P46311 brassica na
35	92.5	4.1	563	CYB_SULAL	P39480 sulfolobus
36	92	4.0	334	ACOD_MESAU	Q64420 mesocricetu
37	91.5	4.0	859	NIA_PICAN	P49050 pichia angu
38	91.5	4.0	524	YE33_SVNY3	P74217 synechocyst
39	91	4.0	893	NIA_LEPMC	P36842 leptosphaer

Matches 83; Conservative 56; Mismatches 162; Indels 88; Gaps 19;

```
Qy 58 LKRPKINPSF-----ELPQAAVNEAQEDFRKLREELIATGMDASPLWYKISTT 110
Db 26 LSRVNTKPPFTVGOLKKAIPHCQFQSLTTSFSYV-----YIDLSEAFIFY-IATT 76
Qy 111 LGLGVLYGFLVVOYQYFI--GAVLLGHYQMGWLSHDICHQTFKKNRW--NNLVGLVF 167
Db 77 YFHLPPQFSLIAWPIYVWLOCLITGV-----WVAHECGHAFSKYQWVDDVVGTL 130
Qy 168 GNLG--QGFSVTCWKDRNNAHSAATVQGHDPDIDNLPPLAWSEDDVTRASPIRKLIQF 225
Db 131 HSTLLVPYFS--WKSHRRHSNTG-----SLDRDEVFPKPKS-KVAFW 172
Qy 226 QQYY-----FLVICILLRFIWCFOCVLTVRSLKDRDQFYRSQYKKEA----- 269
Db 173 SKYLNPNLGRAVSLVLTITIGWPIYAFNV---SGRPVDSFASHYHPYIYSNRRLLI 229
Qy 269 --IGLALHWTALKALHFLFEMPSILTSLLVFFVSEL-VGGFGIAIVFVFN--HYPLEKIGDP 324
Db 230 YVSDVALFSVTSYLRVATLKGWLLCVGYGVPLLIVNGFLVTITLYLQTHFALPHYDSS 289
Qy 325 VMDGHGFSVGQIHETMNTTIRGIITDFFGGLNYQIEHLHWTPLPRHNLTAVSQVEQLC- 384
Db 290 EWD---WLKGAAL-ATMDRDYGLNKVVFHITDTHVAHLFSTMPHYHAMEATNAIKPILG 345
Qy 384 --QKHNLPIYRNPL-----PHEG 398
Db 346 EYQFDPTPFYKALWREARECLYVEPDEG 374
```

RESULT 14

T14269

C:Species: Helianthus annuus (common sunflower)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14269

R:Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J.

submitted to the EMBL Data Library, February 1997

A:Description: Sunflower delta-12 oleate desaturase.

A:Reference number: Z17949

A:Accession: T14269

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-378 <HON>

A:Cross-references: EMBL:U91341; NID:g2290403; PID:g2290404

A:Experimental source: strain Mammoth

C:Function:

A:Description: desaturates oleic acid to linoleic acid

Query Match 6.18; Score 139; DB 2; Length 378;

Best Local Similarity 21.4%; Pred. No. 7.8e-05;

Matches 76; Conservative 52; Mismatches 139; Indels 88; Gaps 19;

```
Qy 58 LKRPKINPSF-----ELPQAAVNEAQEDFRKLREELIATGMDASPLWYKISTT 110
Db 16 LDRVPHAKPFTIGDLKKAIPHCQFQSLTTSFSYVLSDLTITAVL-----YHIATT 67
Qy 111 LGLGVLYGFLVVOYQYFI--GAVLLGHYQMGWLSHDICHQTFKKNRW--NNLVGLVF 160
Db 68 -----YFHHLPPLSSIAWASVWVVGCVLTGV-----WVAHECGHAFSDYQWVD 114
Qy 161 NLVGLVFGNLG--QGFSVTCWKDRNNAHSAATVQGHDPDIDNLPPLAWSEDDVTRASPI 218
Db 115 DTVGFLVHSLLLVPYFS--WKYSHRRHSNTG-----SLERDEV--FVPK 155
Qy 219 SRKLIQFQQYYF-----LVICILLRFIWCFOCVLTVRSLK-DR-----DNQF 259
Db 156 SRSKVPWYSKYFNNTVGRIVSMFVTLTIGWPLYLAFNVGGRPYDRFFACHYVPTSPMYNER 215
Qy 260 YRSQYKKEAIGLALHWTALKALHFLFEMPSILTSLLVFFVSELVGGFGIAIVFVFNH-YPL 318
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Search completed: February 24, 2000, 22:01:39

Job time: 17316 sec

```
Db 216 KRYQIVMSDIGIVI--TSFILRYVAMAKGLVWVICVYGVPLMVVNAFLVLTLYLOHTHP- 273
Qy 319 EKIGDPVWDGHGS--VQGIHETMNRIRGIITDFFGGLNYQIEHHLHWTPLPRHN 371
Db 273 ---GLPHYDSSSEWEWLKGAAL-ATVDRDYGVLENKVFHFHITDTHVVVHLSFSTMPHYN 323

RESULT 15
T11959
fatty-acid desaturase - red alga (Cyanidium caldarium) chloroplast
C:Species: Chloroplast Cyanidium caldarium
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: T11959
R:Gloeckner, G.; Rosenthal, A.; Valentin, K.
submitted to the EMBL Data Library, September 1997
A:Description: Organisation of 46 kb of the Cyanidium caldarium Rk1 plastid genon
A:Reference number: Z17374
A:Accession: T11959
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-287 <GLO>
A:Cross-references: EMBL:AF022186; NID:g2465730; PID:g2465769
A:Experimental source: strain Rk1
C:Genetics:
A:Gene: desa
A:Genome: chloroplast
C:Keywords: Chloroplast
```

Query Match 6.08; Score 136.5; DB 2; Length 287;
Best Local Similarity 23.08; Pred. No. 9.2e-05;
Matches 61; Conservative 34; Mismatches 103; Indels 67; Gaps 14;

```
Qy 113 LGVLGYFLMVOYQYFICAVLLGHYQMGWLSHDICHQTFKKNRWNNLVGLVFGNLQ 172
Db 35 ISIFSIFILHLNSSICFLINLLSLHL--LGTVIHDSHKAADNKYINIFYGHSIAFFL- 92
Qy 173 GFSVTCWKDRNNAHSAATVQGHDPDIDNLPPLAWSEDDVTRASP---ISRKLIQFQQYY 229
Db 92 GFSPFVFSRVHMOHHAYVNDANNDPD-----HEVSTAGPLMLIASRFFYHEVYF 140
Qy 230 FLVICILLRFIWCFOCVLTVRSLKDRDQFYRSQYKKEAIGLALHWTALKALHFLFEMPSI 289
Db 141 F-----QRKLW-----RNKLEIWI--WARTLLICLLFI-AF 169
Qy 290 LTSLLVF-----FVSELVGGFGIAIVV-FMNHYPLEKIGDPVWDGHGFSVGQIHETMNR 343
Db 170 ETNILEYVFKWFCPALVGVGALGCLCFDYLPHYPF-KYTDR-WHN-----SCVYPSKFLN 222
Qy 344 RGIITDFFGGLNYQIEHHLHWTPLP 368
Db 223 LAIF-----GQNYHLVHHLWPSAP 241
```


QY 315 HYP-----LEKIGDPVWDGHSVGOIHETNMIRRGITDWFEGGLNLYQIEHHLWPT 366
 Db 257 HFPDGAKEFKYTDIGEP--KGWY-LRQMLGSANFNAGPALRFMSGNLCHQIEHHLYPD 313
 QY 367 LPRHNLTAVSQVQPOLCKHNLPI 390
 Db 314 LPSNRLHEISVRREVCDYDLPY 337

RESULT 8
 T10789
 omega-6 desaturase, microsomal - upland cotton
 C:Species: Gossypium hirsutum (upland cotton)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
 C:Accession: T10789
 R:Li, Q.; Singh, S.P.; Green, A.; Sharp, P.J.; Marshall, D.R.
 submitted to the EMBL Data Library, March 1999
 A:Description: Isolation and characterisation of two different microsomal omega-6 desaturase
 A:Reference number: 217145
 A:Accession: T10789
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-383 <LIU>
 A:Cross-references: EMBL:Y10112; NID:el393524; PID:e321496
 A:Experimental source: subspecies Deltapine-16
 C:Function:
 A:Description: Involved in production of polyunsaturated lipids
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 6.5%; Score 149; DB 2; Length 383;
 Best Local Similarity 22.8%; Pred. No. 1e-05;
 Matches 82; Conservative 49; Mismatches 156; Indels 76; Gaps 19;

QY 55 FDKLRMPKINPSFEL-----PPQAAVNEAQEDFRKREELIATGMFDASPLWYSYKI 107
 Db 18 FNSLKRVPYSKPPFTLSEIKKAIPPHCFORSVLRSFSLYLYDFILASLF-----YHV 69
 QY 108 STTLGLGVLYFLMVQOMYFI--GAVLLGHVYQOMGLSHDICHQHTFKNRW--NNLVG 164
 Db 70 ATNYFNLPOALSNVAPLWAMGCGILTV-----WVIAHECGHAFSDYQWLDDTVG 123
 QY 165 LVFENGIL--QGFSVTCWKDRHNAHSATNVQGHDPDIDNLP-----LAWSEDDVTRASPI 218
 Db 124 LILHSSLLVPYFS--WKYSRRRHNTSGLSERDEVE--VPKKSGLRWAKHEN--NPP 176
 QY 219 SRKLIQFOQYFLVICILLRFICFCQCVLTVRS-----LKDNDN-QFYR 261
 Db 177 GR-----FLSITITLQTLGWPLYLAFNVAGRPYDRFACHYDPYGPFIQFSDRELQIYI 227
 QY 262 SQYKKEAIGLALHWTALKALFHLFMPSTLTLVFFVSELSVLTSLVGGFGLVAVFMNH-YP-LE 319
 Db 228 S-----DAGVLAVAY---ALRVLAKGVGVVISYGVPLLVNVAFLVMTYLOHTHPSLP 280
 QY 320 KIGDPVWDGHSVGOIHETNMIRRGITDWFEGGLNLYQIEHHLWPTLRHNLTAVSQV 379
 Db 281 HYDSSMD---WMRGAL-STVDRDYGILNKVFNHITDTHVAHLFSTMPHYHAWATKAI 336
 QY 380 EQL 382
 Db 337 KPI 339

RESULT 9
 T15043
 fungal elicitor-induced protein - parsley
 C:Species: Petroselinum crispum (parsley)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15043
 R:Kirsch, C.; Hahlbrock, K.; Somssich, I.E.
 Plant Physiol. 115, 283-289, 1997
 A:Title: Rapid and transient induction of a parsley microsomal delta 12 fatty acid desaturase
 A:Reference number: 218274; MUID:97451781

A:Accession: T15043
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-383 <KIR>
 A:Cross-references: EMBL:U86374; NID:g2501791; PID:g2501792
 C:Genetics:
 A:Gene: ELI12

Query Match 6.5%; Score 147.5; DB 2; Length 383;
 Best Local Similarity 23.1%; Pred. No. 1.4e-05;
 Matches 81; Conservative 45; Mismatches 154; Indels 71; Gaps 16;

QY 54 AFDKLRMPKINPSF-----ELPPQAAVNEAQEDFRKREEL-ITGMFDASPLWYSY 105
 Db 17 AAELKRAPEHEKPPFTIGDLKKAIPAHCFOKSLVTSFYLIQDLFMAYLFVATNYIDQ 76
 QY 106 KISTTLGLGVLYFLMVQOMYFI--GAVLLGHVYQOMGLSHDICHQHTFKNRW--NNLVG 164
 Db 77 YLTPFNYVAAYIAVQ-----GCVLTG-----AMVVGHECHDAFSNYNNINDLVG 124
 QY 165 LVFENGIL--QGFSVTCWKDRHNAHSAT-----NVQGHDPDIDNLP----- 205
 Db 125 LVVHSSLLVPYFS--WKYSRRRHANTQSLNDEDEVVPRFKSNIRNYKLLNN-PPGRV 180
 QY 205 LAWSEDDVTRASPIRKLIQFOQYFLVICILLRFICFCQCVLTVRSKDRDNQFYRSQY 264
 Db 181 LVN-----LTTLLIGFLYLMFNVSCHKYERW-----TSHYDPSPLYSORE 222
 QY 265 KKEAI--GLALHWTALKALFHLFMPSTLTLVFFVSELSV--GGFGTAIVVFNHHPLEK 320
 Db 223 RKEIIVSDIALLAVIYDLYOLVLAKEFAWVFCVYGGPLLVNGMFWLYTLNHTHPSLPY 282
 QY 321 IGPVWDGHSVGOIHETNMIRRGITDWFEGGLNLYQIEHHLWPTLRHN 371
 Db 283 YDSTEND--WLRGALC-TVDRDYGILNKVFNHVCNAHVCHHIFSMPIHYH 329
 RESULT 10
 S77365
 hypothetical protein s111468 - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
 C:Accession: S77365
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Miyajin
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 A:Reference number: S74322; MUID:97061201
 A:Accession: S77365
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-312 <KAN>
 A:Cross-references: EMBL:D90906; GB:AB001339; NID:g1652492; PID:d1018201; PID:g1652492
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Start codon: GTG

Query Match 6.4%; Score 147; DB 2; Length 312;
 Best Local Similarity 20.7%; Pred. No. 1.2e-05;
 Matches 61; Conservative 48; Mismatches 111; Indels 74; Gaps 13;

QY 87 REELIATGMFDASPLWYSYKISTTLGLGVLYFLMVQOMYFI--GAVLLGHVYQOMGLSH 146
 Db 24 KEFLQADGGENPVAMFGTAILMLA-NVFGTWQWGLPHWLCPSCSVLALHLS--GTVII 80
 QY 147 DICHHQTFKNRWNNLVGLVFGNG---LOGFSVTCWKDRHNAHSATNVQGHDPDIDNLP 203
 Db 81 DASHNAHR---NTIINAVLGHGSALMGFAFPFTRVHLOHANNVNDPDP----- 132

[illegible]

delta-6 fatty acid desaturase (EC 1.14.99.-) - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999
C:Accession: JG0180

R:Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.
Biochem. Biophys. Res. Commun. 255, 575-579, 1999

A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid desaturase
A:Reference number: JG0180

A:Accession: JG0180

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-444 <AKI>

A:Cross-references: DBJ:AB021980

C:Superfamily: cytochrome b5 core homology

C:Keywords: oxidoreductase

F:18-94/Domain: cytochrome b5 core homology <CB5>

Query Match 18.8%; Score 428.5; DB 2; Length 444;
Best Local Similarity 29.1%; Pred. No. 1.2e-30;
Matches 118; Conservative 66; Mismatches 178; Indels 43; Gaps 12;

Qy 11 LQMEQTYDVSANWFHPCGAELIENYQGRDATDAFVMVH-----FOEAFDKLKRMPKINP 66

Db 37 LVDRKVNVTWKSQHPGQVRVIGHYAGEDATDAFRAHFDLDFVGVKFLKPLLIGELAP 96

Qy 67 SPELPQAAVNAQEDFRKRLRELIATGMDASPLWYSKISTTGLGVGLVFLMVOYOM 126

Db 97 EEPSSDRGKSSOITEDFRALKTAEDMNLFTKTNHVFLLSHIIVMESIAWFL----S 152

Qy 127 YF-----IGAVLLGMHYQOMGLSHDCHQHTKRNWNNLVGLVFGNGLOGFSVTC 178

Db 153 YFGNGWIPITLITAFVLATSOAQAQGLQHDYGHLSVYKPKNHLVHKFVIGHLKGSANW 212

Qy 179 WKDRNNAHSATNVQGHDPDIDNPLPLAWSDEDDVTRASPI--SRKLIQF-----QOYF 230

Db 213 WNRHFQHAKNIFHKDPDVMNLHVFLGE-----WQPIEGYKPKLKYLPYNNHQHEYFF 267

Qy 231 LV-IGILLRFIWCFCVLTVRSLKDRDNQFYRSQYKKEAIGLALHWTALKALFLHFFMP-- 288

Db 268 LIGPPLIPMYFOYQIIMTM-----IVHKNWVDLAWAVSYIRFITIPFY 314

Qy 288 SILTSLVFFVSELVGGGIAIVFMNHYPLEKIGDPVWDGHSFGVSGQIHTMNRGII 347

Db 315 GILGALLFLNFRFLESHWVYVVTQMNHIVMEIDQEARDD--WFS-SQLTATCNVQSFF 371

Qy 348 TDWFGGLNYQIEHLWPTLPRHNLTAVSQYQEQLCQKHNLPYRNPLPHEGLVILLRYL 406

Db 372 NDWFSGLNFOIEHLFTPMRPHNLHKTAPLVKSLCAKHGIEYQEKPLLRALLDIRSL 430

RESULT 4

T08765

probable delta-6 fatty acid desaturase (EC 1.14.99.-) - human (fragment)

N:Alternate names: protein DKF2p586C201.1

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C:Accession: T08765

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z16471

A:Accession: T08765

A:Molecule type: mRNA

A:Residues: 1-311 <WAM>

A:Cross-references: EMBL:AL050118

A:Experimental source: adult uterus; clone DKF2p586C201

C:Genetics:

A:Note: DKF2p586C201.1

C:Keywords: oxidoreductase

Query Match 13.6%; Score 311.5; DB 2; Length 311;

Best Local Similarity 27.4%; Pred. No. 2.3e-20;

Matches 87; Conservative 53; Mismatches 136; Indels 41; Gaps 9;

Qy 110 TLGLGVGLVFLMVOYQMFVIG-----AVLLGMHYQOMGLSHDCHQHTKRNWNN 160

Db 2 TFGAHIIALESATNTVTFYFGNGWIPITLITAFVLATSOAQAQGLQHDYGHLSVYRPKWN 61

Qy 161 NLVGLVFGNGLOGFSVTCWKDRNNAHSATNVQGHDPDIDNPLPLAWSDEDDVTRASPI-- 219

Db 62 HLVRHFVIGHLKGSANWNNHRRHFQHKAPNIFHKDPDVMNLHVFLGE-----WQPIEV 116

Qy 219 SRKLIQF-----QOYFVLV-ICILLRIFWCQCVLTVRSLKDRDNQFYRSQYKKEAIGL 271

Db 117 GKKLKLYLPYNNHQHEYFFLIGPPLIPMYFOYQIIMTM-----IVHKNWVDL 163

Qy 272 ALHWTALKALFLHFFMP--SILTSLVFFVSELVGGGIAIVFMNHYPLEKIGDPVWDGH 329

Db 164 AWAVSYIRFITIPFYVIGLIGALLFLNFRFLESHWVYVVTQMNHIVMEIDQEARDD-- 222

Qy 330 GFSVQGIHTMNRGIIITDWMFFGGNLTYQIEHLLWPTLPRHNLTAVSQYQEQLCQKHNLP 389

Db 222 WFS-SQLTATCNVQSFFNDWFSGLNFOIEHLFTPMRPHNLHKTAPLVKSLCAKHGIE 280

Query Match

Best Local Similarity

Matches 117; Conservative

70; Mismatches 184; Indels 48; Gaps 11;

Result No.	Score	Query Match	Length	DB ID	Description
1	498.5	21.8	458	2	J69358
2	428.5	18.8	444	2	S60180
3	420	18.4	444	2	delta-6 fatty acid
4	311.5	13.6	311	2	Tl3155
5	239	10.5	359	2	T08765
6	216	9.5	368	2	probable delta-6 f
7	166.5	7.3	427	2	Delta(6)-desaturas
8	149	6.5	383	2	linoleoyl-CoA desa
9	147.5	6.5	383	2	probable desA3 pro
10	147	6.4	312	2	omega-6 desaturase
11	145	6.4	382	2	fungal elicitor-in
12	143.5	6.3	369	2	hypothetical prote
13	140	6.1	387	2	probable omega-6 d
14	139	6.1	378	2	hypothetical prote
15	136.5	6.0	287	2	omega-6 desaturase
16	134.5	5.9	383	2	delta-12 oleate de
17	133.5	5.8	347	2	fatty-acid desatur
18	133	5.8	385	2	omega-6 desaturase
19	132	5.8	350	2	phosphatidylcholin
20	128	5.6	352	2	phosphatidylcholin
21	128	5.6	438	2	fatty-acid desatur
22	127	5.6	349	2	omega-3 fatty acid
23	126.5	5.5	380	2	phosphatidylcholin
24	126.5	5.5	387	2	probable omega-3 f
25	125.5	5.5	431	2	oleate 12-hydroxyl
26	124	5.4	141	2	omega-3 fatty acid
27	120	5.3	383	2	hypothetical prote
28	120	5.3	351	2	omega-3 fatty acid
29	120	5.3	383	2	phosphatidylcholin
30	120	5.3	382	2	Deitai2 oleate des
31	118	5.2	379	2	omega-6 fatty acid
32	117	5.1	453	2	omega-3 fatty acid
33	117	5.1	447	2	omega-3 fatty acid
34	116.5	5.1	460	2	n-6 fatty acid des
35	114	5.0	380	2	omega-3 fatty acid
					Desat3 fatty acid

QY	11	LQLM	EQTYDVSAWVNFHPGGA	IIENYQGRDATDAFVMVHFOEADFKLRMPKINPSFEL	70
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	35	ISIL	GVYVNTWAKEHPGGDAP	LINLAGQDVTDAFIAFPGTAW---KHLDKLFTGYHL	91
		:	:	:	:
		:	:	:	:
		:	:	:	:
QY	71	PQAA	VAWEAQEDFRKLR	REELIATGHDASPLWYSYK---ISTLGLGVLYFLMVQYQMY	127
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	92	-KDY	QVSDISRDYKLA	SEFAKAGFERKKGHGYIYSLCFVSLLSACVYGVLYSGSFWH	150
		:	:	:	:
		:	:	:	:
		:	:	:	:
QY	128	FIGA	VLGHMHYQOMGWL	SHDICHOTEFKNNNNNLVGLVFGWGLQGSFYTCWKDRHNAHH	187
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	151	MUSG	ALLGLAWQIAYL	GHDAGYOMATRGWKNKTAGIFIGNICIGISTANWKWTHNAHH	210
		:	:	:	:
		:	:	:	:
		:	:	:	:
QY	188	SATN	VQGHDPDNDNPL	PLAWSE---DDVTRA-----SPISRKLIOFOQY-YFLVIGCI	235
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	211	IACN	SLDYDPDLOHLP	MLAVSSKLENSITSVFYGRQLTFDPLARFVSQYHLYYPIMCV	270
		:	:	:	:
		:	:	:	:
		:	:	:	:
QY	236	--LLR	FIWCFQCVLTVR	SLUKDRNOFYRSQYKKEAIGLALHWTALKALF--HLEFWPSILT	291
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	271	ARNV	LYLOITLLLSK	RKIPDRG-----LNILGTLIWTFPPLVSRLPNNPERVA	321
		:	:	:	:
		:	:	:	:
		:	:	:	:
QY	292	SLLV	FVFSVSLVGGF	IAIVVF-MNHVPLE-KGDPWDWGHGFSVQIHEHTAIRGIITD	349
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	322	FVLV	FSCVT-----GIQ	HOIQTILNFHSGDVVYGGPP--KGDNNFEKQTRGTIDACSSWMD	374
		:	:	:	:
		:	:	:	:
		:	:	:	:
QY	350	WFFG	GLNYOIEHHLNPT	LRPHNLTAVSQYQVEOLCOKHNLPRYNPLPHEGLVILLRYLAVE	409
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	375	WFFG	GQFOLEHHLPR	LRPCHRLRSISPCRELCKKYNLPYVSLFYDANVTTLTLRTPA	434
		:	:	:	:
		:	:	:	:
		:	:	:	:
QY	410	ARMA	413		
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	435	ALQA	438		
		:	:	:	:
		:	:	:	:
		:	:	:	:

RESULT 2

IG0180

[illegible]

ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

Query Match	24.7%	Score 565;	DB 13;	Length 355;
Best Local Similarity	34.9%	Pred. No. 9e-52;		

Db 368 FFTQIITGRDVHPLFANFTGGLNYQIEHHLFSPMRHNSKIQPAVETLCKKNVRY 427
 QY 391 RNPPLHEGLVILLRLYLAUFARMAEKOPA-----GKA 421
 Db 428 HTTGMIEGTA-----EVSRLNEVSKAASKMGKA 456

RESULT 13
 US-09-377-475-4
 ; Sequence 4, Application US/09377475
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUITZON, DEBORAH
 ; APPLICANT: MUKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LIMBACH & LIMBACH L.L.P.
 ; STREET: 2001 FERRY BUILDING
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/377.475
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARD, MICHAEL R.
 ; REGISTRATION NUMBER: 38,651
 ; REFERENCE/DOCKET NUMBER: CGAB 102
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)433-4150
 ; TELEFAX: (415)433-8716
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 457 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-377-475-4

Query Match 27.2%; Score 622; DB 17; Length 457;
 Best Local Similarity 32.7%; Pred. No. 1e-57;
 Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;

QY 2 KSKQALSPQLM--EQYDYSANVNFHFGAGIEIYQGRDATDAFVMHFQEAFLK 59
 Db 23 EGKKDAEAPFLMIIDNKVYDVRFPDHPGGS-VILTHVGKDGTDVDFHPEAAWETL- 81
 QY 60 RMPKINSPFELPPQAAVNEAQEDF-----RKLRELIATGMFDASPLWYSYKISTT 110
 Db 81 -----ANFYV---GDIDESDRTKNDPFAAEVRKRLTFLQSLGYDSSKAYIAFKVSN 131
 QY 111 LGLGLVGYFLMVQYQM-----YFAGVLLGMHYQOMGLSHDICHQPFKRNKNNNLVGL 165
 Db 132 LCINGLSTVIVAKWGQSTLANVLISAALLGLFWQCQGLHNDFLHHQVDFQDFWGLDPLGA 191
 QY 166 VFGNGLGQFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDDVDVTRASPI----- 219
 Db 192 FLGGVCQCGFSSSMKKDKHNTHAAPNVHVEDPDIDTHTPLLTWSHALEMFSDVPDEELTR 251

QY 219 --SRKLIQOQYFLVICILLRFINCFQCVLTVRSUKDRDNQOFYRSQYK-----EAIG 270
 Db 252 MMSRFMVLNQWTFYFPLSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
 QY 271 LALHTLTKALFHLFEMPSILTSILVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDGHC 330
 Db 308 LAHWHTWYLATMFLFKDPVNMVYFLVLSQAVCGNLAIVFLNHNMGMPVISKEEAVDMD 367
 QY 331 FSVGQIHETMNIIRGITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQYVEQLCQKHNLPY 390
 Db 368 FFTQIITGRDVHPLFANFTGGLNYQIEHHLFSPMRHNSKIQPAVETLCKKNVRY 427
 QY 391 RNPPLHEGLVILLRLYLAUFARMAEKOPA-----GKA 421
 Db 428 HTTGMIEGTA-----EVSRLNEVSKAASKMGKA 456

RESULT 14
 US-08-834-033A-6
 ; Sequence 6, Application US/08834033A
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUITZON, DEBORAH
 ; APPLICANT: MUKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
 ; STREET: 2001 FERRY BUILDING
 ; CITY: SAN FRANCISCO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/834.033A
 ; FILING DATE: 11-APR-1997
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARD, MICHAEL R.
 ; REGISTRATION NUMBER: 38,651
 ; REFERENCE/DOCKET NUMBER: CGAB-300.USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 433-4150
 ; TELEFAX: (415) 433-8716
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 355 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-834-033A-6

Query Match 24.7%; Score 565; DB 12; Length 355;
 Best Local Similarity 34.9%; Pred. No. 9e-52;
 Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;

QY 82 DFRKRLRELIATGMFDASPLWYSYKISTTGLGLVGLFVLMVQYQM-----YFAGVLLGM 136
 Db 1 EVKRLRTLFSGLGYDSSKAYIAFKVSNLCIWLSTVIVAKWGQSTLANVLISAALLGL 60
 QY 137 HYQOMGLSHDICHQPFKRNKNNNLVGLVFGNGLGQFSVTCWKDRHNAHSATNVQGH 196

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,985
FILING DATE: 24-OCT-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/834,033
FILING DATE: 11-APR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/833,610
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.128.01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-936-985-15

```

```

Query Match      27.2%; Score 622; DB 13; Length 457;
Best Local Similarity 32.7%; Pred. No. 1e-57;
Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;

QY  2 KSKRQALSPQLM--EQTYDVSANVNFHFGGAEIENYQGRDATDAFMVHFOEAFDKLK 59
DB  23 EGKDAEAPFLMIIDNKVDVREFVDPDPGGS-VILTHVGKOGTDFVDFHPEAAWETL- 81
QY  60 RMPKINPSFELPPQAAVNAEQEDF-----RKLEELIATGMFASPLWYSYKISTT 110
DB  81 -----ANFV---GDIDESDRDIKNDFFAAEVKRLTLFQSLGYDSSKAYYAFKVSFN 131
QY  111 LGLGVLYFLMVOYQ-----YFIGAVLGMHYOQMGWLSHDICHOTFKNRNWNVLVL 165
DB  132 LCINGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGGLAHDLFHHQVQDFRFGDLFGA 191
QY  166 VFGNGLGQFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPI----- 219
DB  192 FLGGVCGQFSSSWKDKHNTHAAPNVHVEDPDIDTHPLTWSEHALEMFSVDPDELTR 251
QY  219 --SRKLIQOQYFYFLVICILLRIFWCQVLTVRSKDRDNQYRSQYK-----EAIG 270
DB  252 MWSRFVNLQNTWFFYFIFLSFARLSWCLQSILFVLP-----NGQAKPSSGARVPISLVEQLS 307
QY  271 LALHWTLKALFHLFFMPSILTSLLVFFVSELVGGFGIAIVFVNHNHYPLEKIGDPVWDG 330
DB  308 LAHWHTWYLATMFLFKDPVNMVLYFLVSOAVCGNLLAIVFSLNHNHMPVISEEAVDMD 367
QY  331 FSVGQIHTMNIIRGIITDWFGLNLYQIEHHLWPLTPRNLTAVSQVQEQLOKKNLPY 390
US-09-377-452-4
; Sequence 4, Application US/09377452

```

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GENERAL INFORMATION:
APPLICANT: KNUTSON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: LIMBACH & LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/377,452
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)433-4150
TELEFAX: (415)433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-377-452-4

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```

Query Match      27.2%; Score 622; DB 17; Length 457;
Best Local Similarity 32.7%; Pred. No. 1e-57;
Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;

QY  2 KSKRQALSPQLM--EQTYDVSANVNFHFGGAEIENYQGRDATDAFMVHFOEAFDKLK 59
DB  23 EGKDAEAPFLMIIDNKVDVREFVDPDPGGS-VILTHVGKOGTDFVDFHPEAAWETL- 81
QY  60 RMPKINPSFELPPQAAVNAEQEDF-----RKLEELIATGMFASPLWYSYKISTT 110
DB  81 -----ANFV---GDIDESDRDIKNDFFAAEVKRLTLFQSLGYDSSKAYYAFKVSFN 131
QY  111 LGLGVLYFLMVOYQ-----YFIGAVLGMHYOQMGWLSHDICHOTFKNRNWNVLVL 165
DB  132 LCINGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGGLAHDLFHHQVQDFRFGDLFGA 191
QY  166 VFGNGLGQFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSEDDVTRASPI----- 219
DB  192 FLGGVCGQFSSSWKDKHNTHAAPNVHVEDPDIDTHPLTWSEHALEMFSVDPDELTR 251
QY  219 --SRKLIQOQYFYFLVICILLRIFWCQVLTVRSKDRDNQYRSQYK-----EAIG 270
DB  252 MWSRFVNLQNTWFFYFIFLSFARLSWCLQSILFVLP-----NGQAKPSSGARVPISLVEQLS 307
QY  271 LALHWTLKALFHLFFMPSILTSLLVFFVSELVGGFGIAIVFVNHNHYPLEKIGDPVWDG 330
DB  308 LAHWHTWYLATMFLFKDPVNMVLYFLVSOAVCGNLLAIVFSLNHNHMPVISEEAVDMD 367
QY  331 FSVGQIHTMNIIRGIITDWFGLNLYQIEHHLWPLTPRNLTAVSQVQEQLOKKNLPY 390
US-09-377-452-4
; Sequence 4, Application US/09377452

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;
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-574-2

Query Match          27.6%  Score 631; DB 17; Length 457;
Best Local Similarity 33.0%  Pred. No. 1.1e-58;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY  2 KSKQALSPQLM--EQTYDVSAMVNFHPGGAETIENYQGRDATDAFMMHFQEAFLK 59
DB 23 EGKDAEAPFLMIIDNKVDYREFVDPHGG--VILTHVGKDGTDVDTFHPAAWETL- 81
QY  60 RMPKINPSPQLM--EQTYDVSAMVNFHPGGAETIENYQGRDATDAFMMHFQEAFLK 110
DB 81 -----ANFYV---GDIDESDRDKNDFAAEVVKRLTLFQSLGYDSSKAYIAFKVSFN 131
QY  111 LGLGVLYFLMVOYOM-----YFICAVLLGMHYQOMGWLSDHICHQHTFKRNNNNLVL 165
DB 132 LCITWGLSTVIVAKWGQSTLANVLNLSAALLGLFWQCGWLAHDFLHQVQDFRFGDLFGA 191
QY  166 VFGNGLOGFSVTCWKDRNNAHSAATNVQGHDPDIDNLPPLAWSDDVTRASPI----- 219
DB 192 FLGGVCGCFSSWKKDKHNTHAAPNVHVEDPDIDTHTPLTWSEHALEMFSVDPDELTR 251
QY  219 --SRKLIQFOQYFLVICILLRFTWCQCVLTVRSKDRDNQFYSYKK-----PAIG 270
DB 252 MWSRFVNLQNTWFFPILSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
QY  271 LALHWTLKALFLHFLFMPISILTSLLVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDHG 330
DB 308 LAMHTWYLATMFLFKDPVNMVLYFLVSAVCGNLLAIVFSLNHNMPVISKEEAVDMD 367
QY  331 FSVGQIHTMNIIRGIITDWFQGLNLYQIEHLLMPTLPRNLTAVSYQVQLCKHNL 390
DB 368 FFTKQIITGRDVHPGLFANFTGGLNYQIEHLLFSPMPRNFESKIQPAVETLCKKNVRY 427
QY  391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB 428 HTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 10
US-08-834-033A-14
; Sequence 14, Application US/08834033A
; GENERAL INFORMATION:
; APPLICANT: KNOTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:

```

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;
; APPLICATION NUMBER: US/08/834.033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-033A-14

Query Match          27.2%  Score 622; DB 12; Length 457;
Best Local Similarity 32.7%  Pred. No. 1e-57;
Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;

QY  2 KSKQALSPQLM--EQTYDVSAMVNFHPGGAETIENYQGRDATDAFMMHFQEAFLK 59
DB 23 EGKDAEAPFLMIIDNKVDYREFVDPHGG--VILTHVGKDGTDVDTFHPAAWETL- 81
QY  60 RMPKINPSPQLM--EQTYDVSAMVNFHPGGAETIENYQGRDATDAFMMHFQEAFLK 110
DB 81 -----ANFYV---GDIDESDRDKNDFAAEVVKRLTLFQSLGYDSSKAYIAFKVSFN 131
QY  111 LGLGVLYFLMVOYOM-----YFICAVLLGMHYQOMGWLSDHICHQHTFKRNNNNLVL 165
DB 132 LCITWGLSTVIVAKWGQSTLANVLNLSAALLGLFWQCGWLAHDFLHQVQDFRFGDLFGA 191
QY  166 VFGNGLOGFSVTCWKDRNNAHSAATNVQGHDPDIDNLPPLAWSDDVTRASPI----- 219
DB 192 FLGGVCGCFSSWKKDKHNTHAAPNVHVEDPDIDTHTPLTWSEHALEMFSVDPDELTR 251
QY  219 --SRKLIQFOQYFLVICILLRFTWCQCVLTVRSKDRDNQFYSYKK-----PAIG 270
DB 252 MWSRFVNLQNTWFFPILSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
QY  271 LALHWTLKALFLHFLFMPISILTSLLVFFVSELVGGFGIAIVFMNHYPLEKIGDPVWDHG 330
DB 308 LAMHTWYLATMFLFKDPVNMVLYFLVSAVCGNLLAIVFSLNHNMPVISKEEAVDMD 367
QY  331 FSVGQIHTMNIIRGIITDWFQGLNLYQIEHLLMPTLPRNLTAVSYQVQLCKHNL 390
DB 368 FFTKQIITGRDVHPGLFANFTGGLNYQIEHLLFSPMPRNFESKIQPAVETLCKKNVRY 427
QY  391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB 428 HTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 11
US-08-956-985-15
; Sequence 15, Application US/08956985
; GENERAL INFORMATION:
; APPLICANT: KNOTZON, DEBORAH
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

```

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Db 81 -----ANFYV---GDIDESDRDKNDFAAEVRKRLTLFOSLGYDSSKAYIAFKVSFN 131
Qy 111 LGLGVLYFLMVQYOM-----YFYGAVLLGMHYOQMGWLSHDICHGHTQFFKRNKNNLVGL 165
Db 132 LCTWGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHHQVQDFRFGDLEGA 191
Qy 166 VFGNGLOGFSVTCWKORNAHHSATNVQGHDPDIDNPLPPLAWSDEDDVTRASPI----- 219
Db 192 FLGVCVCGFSSWKKHNTHAAPNVHGEDPDIDTHPLLTWSEHALEMFSVDPDEELTR 251
Qy 219 --SRKLQFOQYFLVICILLRFTWCFCQVLTVRSKDRDNQFYSQYKK-----EAIG 270
Db 252 MWSRFVNLQWTFYFPLSFARLSWCLQSILFVLP-----NGOAHKPGSGARVPIISLVEOLS 307
Qy 271 LALHWTALKALPHLFPMFSILTSLLVFFVSELVGGFIAVVMNHYPLEKIGDPVWDGHC 330
Db 308 LAHWTWYLATMFLFIKDPVNMVLYFLVQAVCGNLLAIVFSLNHNHGMPIVSKKEAVDMD 367
Qy 331 FSVGQIHETNIRGIIITDWFEGGLNYOIEHHLWPTLPRHNLTAVSQVQEOQLCKHNLPL 390
Db 368 FFTKQITGRDVHPGLFANWFTGGLNYOIEHHLFSPMRHNFESKIOPAVETLCKKYNRY 427
Qy 391 RNPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
Db 428 HTTGMIEGTA-----EVSRLNEVSKAASKMGKA 456

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RESULT 8
US-09-363-526-2
: Sequence 2, Application US/09363526
: GENERAL INFORMATION:
: APPLICANT: KNUTZON, DEBORAH
: APPLICANT: MURKERJI, PRADIP
: APPLICANT: HUANG, YUNG-SHENG
: APPLICANT: THURMOND, JENNIFER
: APPLICANT: CHAUDHARY, SUNITA
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
: TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
: STREET: 2001 FERRY BUILDING
: CITY: SAN FRANCISCO
: STATE: CA
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/363,526
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: WARD, MICHAEL R.
: REGISTRATION NUMBER: 38,651
: REFERENCE/DOCKET NUMBER: CGAB-201 USA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 433-4150
: TELEFAX: (415) 433-8716
: TELEX: N/A
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 457 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-363-526-2

```

```

Query Match 27.68; Score 631; DB 17; Length 457;
Best Local Similarity 33.04; Pred. No. 1.le-58;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

Qy 2 KSKRQALSPLQLM--EOTYDVSAMVNFHPGGAETIENVQGRDATDAFVMVHFQEAFLK 59
Db 23 EGKADAPFLMIIDNKVYDVREVPDPHGG--VILTHVGKDGTDVFTTFPEAAWETL- 81
Qy 60 RMPKINPSFELPPOAAVNEAQEDF-----RKREELIATGMFASPLMYSYKISTT 110
Db 81 -----ANFYV---GDIDESDRDKNDFAAEVRKRLTLFOSLGYDSSKAYIAFKVSFN 131
Qy 111 LGLGVLYFLMVQYOM-----YFYGAVLLGMHYOQMGWLSHDICHGHTQFFKRNKNNLVGL 165
Db 132 LCTWGLSTVIYAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHHQVQDFRFGDLEGA 191
Qy 166 VFGNGLOGFSVTCWKORNAHHSATNVQGHDPDIDNPLPPLAWSDEDDVTRASPI----- 219
Db 192 FLGVCVCGFSSWKKHNTHAAPNVHGEDPDIDTHPLLTWSEHALEMFSVDPDEELTR 251
Qy 219 --SRKLQFOQYFLVICILLRFTWCFCQVLTVRSKDRDNQFYSQYKK-----EAIG 270
Db 252 MWSRFVNLQWTFYFPLSFARLSWCLQSILFVLP-----NGOAHKPGSGARVPIISLVEOLS 307
Qy 271 LALHWTALKALPHLFPMFSILTSLLVFFVSELVGGFIAVVMNHYPLEKIGDPVWDGHC 330
Db 308 LAHWTWYLATMFLFIKDPVNMVLYFLVQAVCGNLLAIVFSLNHNHGMPIVSKKEAVDMD 367
Qy 331 FSVGQIHETNIRGIIITDWFEGGLNYOIEHHLWPTLPRHNLTAVSQVQEOQLCKHNLPL 390
Db 368 FFTKQITGRDVHPGLFANWFTGGLNYOIEHHLFSPMRHNFESKIOPAVETLCKKYNRY 427
Qy 391 RNPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
Db 428 HTTGMIEGTA-----EVSRLNEVSKAASKMGKA 456

RESULT 9
US-09-363-574-2
: Sequence 2, Application US/09363574
: GENERAL INFORMATION:
: APPLICANT: KNUTZON, DEBORAH
: APPLICANT: MURKERJI, PRADIP
: APPLICANT: HUANG, YUNG-SHENG
: APPLICANT: THURMOND, JENNIFER
: APPLICANT: CHAUDHARY, SUNITA
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
: TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
: STREET: 2001 FERRY BUILDING
: CITY: SAN FRANCISCO
: STATE: CA
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/363,574
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: WARD, MICHAEL R.
: REGISTRATION NUMBER: 38,651
: REFERENCE/DOCKET NUMBER: CGAB-202 USA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 433-4150
: TELEFAX: (415) 433-8716

```

[illegible]

RESULT 6
US-09-087-578-4
; Sequence 4, Application US/09087578
; GENERAL INFORMATION:
; APPLICANT: KOPCHIK, JOHN J.
; APPLICANT: KELDER, BRUCE
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: KIRCHNER, STEPHEN J.
; APPLICANT: MUKERJI, PRADIP
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
; TITLE OF INVENTION: PRODUCTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,578
; FILING DATE: 29-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-03348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-09-087-578-4

Query Match          27.6%; Score 631; DB 14; Length 457;
Best Local Similarity 33.0%; Pred. No. 1.le-58;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY      2 KSKRQALSPLOLM--EOTYDYSAWNVHPGCAEIIENYQGRDATDAFVMWHFOAFDKLK 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      23 EGKKDAEAPFLMIITDNKYDVREYFVDPHGGG-VILTHVGKGDVDFDTFPEAAWETL- 81
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      60 RMPKINSEFELPPOAAVNEAQEDP-----RKLREELIATGMFASPASLPWYSVKISTT 110
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      81 -----ANFYV---GDIDESDRDIKNDDFAAEVRKLTFLQSLGYGYDSSKAYAYAFKYSFN 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      111 LGLGVLYGYFLMVQYOM-----YFTGAVLLGHYQOMGWLSHDICHCHOTFFKNRNNNVL 165
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      132 LCINGLSTVIVAKWGOSTSTLANVLSAALLGLFWQCCGLAHDFLRHQVFQDFRWGDLFGA 191
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      166 VFGNGLOGFVTCVKDRHNAHSHATNYOGHDPDIDNLPPLAWSDEDDYTRASPI----- 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      192 FLGVCVCGFGSSWKKRNTTHAAPNVHGEPDIDTPLLTWSHALEMFSVDPDEELTR 251
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      219 --SRKLIQFOQYYFLVICILLRFIWCQCQVLTVRSKDRDNQFYRSQYKK-----EAIG 270
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      252 MWSRFVNLQNTWFVFPILSPFARLSWCQLSILFVLP----NGQAHKPSGARVPISLVEQLS 307
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      271 LALHWTLKALFLHFLFFPMSILTSLVPFVSELVGGFGTAIVVFNNHYPLEKIGDPWDGHC 330
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      308 LAMHWTYLATMELFIKDPVNNMLVFLVSOAVCGNLLAIVFSLNHNNGMPVISKEEAYDMD 367
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      331 FSVGQIHETNWRIGITDFFGGLNYQIEHHLWPTLPRLNLTAVSYQVQECOLCKHNLPL 390
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      368 FFTQKIITGRDVPGLFANFTGGLNYQIEHHLFSPNPRHNFSKIQPAVETLCKKNVRY 427
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      391 RNPDPHEGLVILLRYLAVFARMAEKQPA-----GKA 421
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      428 HTTGMTEGTA-----EVFSRLNEVSKAASKMGKA 456
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT      7
US-09-351-525-4
; Sequence 4, Application US/09351525
; GENERAL INFORMATION:
; APPLICANT: Kopchick, John J.
; APPLICANT: Kelder, Bruce
; TITLE OF INVENTION: Mammalian Cells Expressing Desaturases and Elongases
; FILE REFERENCE: OHU-03765
; CURRENT APPLICATION NUMBER: US/09/351,525
; CURRENT FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Mortierella Alpina
US-09-351-525-4

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Query Match      27.6%; Score 631; DB 17; Length 457;
Best Local Similarity 33.0%; Pred. No. 1.1e-58;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY      2 KSKRQALPLQLM--EQTYDVSAWNFNHFGGAEIENYQGRDATAFYVMYHFOEAPDKLK 59
DB      23 EGKKDAEAPFLMIIDNKVYDVREYFDPHGGGS-VILTHVGKDGTDVDFTHPEAAWETL- 81
QY      60 RMPKINPSFELPPQAAVNEAQEDF-----RKLRRELIATGMFDSAPLWYSYKISTT 110

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Db 308 LAMHTWYLATWELFIKDPVNLVYFLVSOAVCGNLLAIVFSLNHNMPVISEEAVDMD 367
 Qy 331 FSVGOIHETMNRIRGITDWFEGGLNYQIEHHLWPTLPRLHNTAVSYQVQEQCQKHNLPY 390
 Db 368 FETKQIITGRDHPGLFANFTGGLNYQIEHHLFSPMRHNFSKIOPAVETLCKKYNVRY 427
 Qy 391 RNPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
 Db 428 HTGMIEGTA-----EVFSRLNEVSKAAKMGKA 456

RESULT 4
 US-08-956-985-2
 ; Sequence 2, Application US/08956985
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUTZON, DEBORAH
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 ; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08956,985
 ; FILING DATE: 24-OCT-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/834,033
 ; FILING DATE: 11-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/833,610
 ; FILING DATE: 11-APR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.128.01US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 328-4400
 ; TELEFAX: (650) 328-4477
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 457 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-956-985-2

Query Match 27.6%; Score 631; DB 13; Length 457;
 Best Local Similarity 33.0%; Pred. No. 1.le-58;
 Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

Qy 2 KSKROALSPLOLM--EQTVDVSAWVNFHPGGAETIENYQGRDATDAFVMVHFOEAPDKLX 59
 Db 23 ECKKDAEAPFLMIDNKVDYVREFFVDPHGGGS-VILTHVGKGDGVDVDFTHPEAAWETL- 81
 Qy 60 RMPKINPSPQLPQAANVEAQDF-----RKREELIATGMFASPLWYSYKISTT 110
 Db 81 -----ANFVV---GDIKESDRIDKNDFFAAEVRKRLTLFQSLGYDSSKAYVAFKVSFN 131
 Qy 111 LGGLVGLYFLMVOYOM-----YFIGAVLLGMHYQOMGLSHDCHHOTTFRNNNNVGL 165

Db 132 LCINWGLSTVIVAKWGOTSTLANVLSAALLGLFWQCGWLAHDFLHHQVFDQRFWGDLFGA 191
 Qy 166 VFGNGLOQSVTCWDRHNAHHSATNVQCHDDPDIDNLPLAWSEDDYTRASPI----- 219
 Db 192 FLGGVCOGFSFSSWMDKHNTHAAPNVHGEDPDIDTHPLTWSEHALEMFSVDYDDELTR 251
 Qy 219 --SRKLIQFQQXYELVICILLRFIMCFQCVLTVRSLKDRDNQFYRSQYKK-----EAIG 270
 Db 252 MMSRFVNLQNTWFFYFPIILSFARLSWCLQSLILFVLP-----NGQAHKSGGARVPISLVEQLS 307
 Qy 271 LALHWTLKALFLHFFEMPSILTSLLVFFVSELVGGFGIAIVFNMNHYPLEXIGDPVWDG 330
 Db 308 LAMHTWYLATWELFIKDPVNLVYFLVSOAVCGNLLAIVFSLNHNMPVISEEAVDMD 367
 Qy 331 FSVGOIHETMNRIRGITDWFEGGLNYQIEHHLWPTLPRLHNTAVSYQVQEQCQKHNLPY 390
 Db 368 FETKQIITGRDHPGLFANFTGGLNYQIEHHLFSPMRHNFSKIOPAVETLCKKYNVRY 427
 Qy 391 RNPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
 Db 428 HTGMIEGTA-----EVFSRLNEVSKAAKMGKA 456

RESULT 5
 US-08-956-985A-2
 ; Sequence 2, Application US/08956985A
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUTZON, DEBORAH
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 ; STREET: P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0039
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08956,985A
 ; FILING DATE: 24-OCT-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/834,033
 ; FILING DATE: 11-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/833,610
 ; FILING DATE: 11-APR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE128.01US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 328-4400
 ; TELEFAX: (650) 328-4477
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 457 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-956-985A-2

Query Match 27.6%; Score 631; DB 13; Length 457;
 Best Local Similarity 33.0%; Pred. No. 1.le-58;


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Db 181 DRNAHRSATNVCHDHPDIDNLPPLAWSDDVTRASPISRKLIQFQQYFLVICLLRFI 240
QY 241 WCFQCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTALKALFLHFMPSILTSLLVFFVSE 300
Db 241 WCFQCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTALKALFLHFMPSILTSLLVFFVSE 300
QY 301 LVGGFGIAIVFNMHYPLEKIGDPVWDGHSVGOIHETMNRIRGIITDFFGGLNYQIE 360
Db 301 LVGGFGIAIVFNMHYPLEKIGDPVWDGHSVGOIHETMNRIRGIITDFFGGLNYQIE 360
QY 361 HHLWPTLPRNLTAHSVQVEQLCQKHNLPYRNPLPHEGLVILLRYLAVFARMAEKQPAKG 420
Db 361 HHLWPTLPRNLTAHSVQVEQLCQKHNLPYRNPLPHEGLVILLRYLAVFARMAEKQPAKG 420
QY 421 AL 422
Db 421 AL 422

RESULT 2
PCT-US99-28655-2
; Sequence 2, Application PC/TUS9928655
; GENERAL INFORMATION:
; APPLICANT: Browne, John et al.
; TITLE OF INVENTION: Desaturases and Methods of Using Them for Synthesis of
; FILE REFERENCE: 53860
; CURRENT APPLICATION NUMBER: PCT/US99/28655
; EARLIER FILING DATE: 1999-12-06
; EARLIER FILING DATE: 60/111,301
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
PCT-US99-28655-2
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Query Match 28.0%; Score 638.5; DB 1; Length 447;
Best Local Similarity 37.1%; Pred. No. 1.6e-59;
Matches 145; Conservative 64; Mismatches 151; Indels 31; Gaps 9;

QY 27 HPGGAEIENYQGRDATDAFVNVH--FOEAFDKLRMPKINPSF--ELP-----PQAAYN 77
Db 30 HPGGS-AITTYKNMDATTVFHTGSKAYQWLTELKKECPQEPEDIKDDPIKGID 88
QY 78 EA-----QEDFKRLRELIATGMFASPLWYSYKISTTILGLVGLVGLMW 122
Db 89 DYNMGTENISEKRSQAQINSFTDLRMVRAEGLMDGSPLEYIKLLETITILFAYL-- 147
QY 123 QYOMTFI-GAVLGMHYQMGWLSHDICHHQTFKRNWNVNLVGLVFGNGLQGSFVTCWKD 181
Db 147 QYHTYLPAILGVAQWGLWLIHEFAHQLFKRYNDLASYFVGNFLQGSFSGGWKE 206
QY 182 RINAHSATNVCHDHPDIDNLPPLAWSDDVTRASPIS--RKLIQFQQYFLVICILLRF 239
Db 207 QINVHAATNVVGRDGLDLPFYATVAEHLNNYSQDSWMTLFRQHVHTFMPFLRL 266
QY 240 IWCFCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTALKALFLHFMPSILTSLLVFFVS 299
Db 267 SWLLASIFVSPOMPHYDYIRNTAIYEQVGLSLHAW--SLGOLYFLPDWSTRIMFFLV 325
QY 300 ELVGGFGIAIVFNMHYPLEKIGDPVWDGHSVGOIHETMNRIRGIITDFFGGLNYQI 359
Db 326 HLVGFLSHVTVFNHYSVEKFAKSSNINVAQIQTIRNRPGRFIDLWGLGLNYOI 385
QY 360 EHLWPTLPRNLTAHSVQVEQLCQKHNLPY 390
Db 386 EHLWPTLPRNLTAHSVQVEQLCQKHNLPY 416
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RESULT 3
US-08-834-033A-2
; Sequence 2, Application US/08834033A
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; NUMBER OF INVENTIONS: 26
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-834-033A-2
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Query Match 27.6%; Score 631; DB 12; Length 457;
Best Local Similarity 33.0%; Pred. No. 1.1e-58;
Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKROALSPQLM--EQTYDVSANVNFHPGGAEIENYQGRDATDAFVNVHFOEAFDKL 59
Db 23 EGKKADEAPFLMIIDNKVYDREVPDPHPPGS-VILTHVYKGDGTDVDFHPPEAAWETL- 81
QY 60 RMPKINPSFELPPQAQVNEAQEDF-----RKLRELIATGMFASPLWYSYKIST 110
Db 81 -----ANFYV---GDIDESDRDIXNDPFAAEVRKRLTLFQSLGYDYSKAYAFKVSFN 131
QY 111 LGLVGLVGLVVOYQM-----YFIGAVLGMHYQMGWLSHDICHHQTFKRNWNVNLVGL 165
Db 132 LCINGLSTIVAKWQSTLANVLSNALLGLFWQCGGLAHDFLHHQVQDFRFGDLFGA 191
QY 166 VFGNGLQGSFVTCWKDRHNAHSAITNVQGHDPDIDNLPPLAWSDDVTRASPIS----- 219
Db 192 FLGGVCGQGSFSSWKKDKHNTTHAAPNVHGEDPDIDTHPLLTWSEHALENFSDVPDELTR 251
QY 219 --SRKLIQFQQYFLVICILLRFIWCFCQVLTVRSKDRDNQFVRSQYK-----EATG 270
Db 252 MNSRFVNLNQTWFYFPIILSFARLSWCLQSILFVLP---NGQAHKPSGARVPISLVEQLS 307
QY 271 LALHWTALKALFLHFMPSILTSLLVFFVSELVGGFGIAIVFNMHYPLEKIGDPVWDGHS 330
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GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2000, 04:47:15 ; Search time 78.22 Seconds
(without alignments)
548.480 Million cell updates/sec

Title: PCT-US99-28655-4
Perfect score: 2283
Sequence: 1 MKSKRQALSPQLMEQTYDV.....LRYLAVFARMAEKOPAGKAL 422

Scoring table: BLOSUM62

Searched: 645694 seqs, 101663753 residues

Database : Pending_Patents_AA:*

Word size : 0

Number of hits that pass the threshold : 645694
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4: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
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22: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
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24: /cgn2_6/ptodata/1/paa/US094_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	2283	100.0	422	1 PCT-US99-28655-4
2	638.5	28.0	447	1 PCT-US99-28655-2
3	631	27.6	457	12 US-08-834-033A-2
4	631	27.6	457	13 US-08-956-985-2
5	631	27.6	457	13 US-08-956-985A-2
6	631	27.6	457	14 US-09-087-578-4
7	631	27.6	457	17 US-09-351-525-4
8	631	27.6	457	17 US-09-363-526-2
9	631	27.6	457	17 US-09-363-574-2
10	622	27.2	457	12 US-08-834-033A-14
11	622	27.2	457	13 US-08-956-985-15
12	622	27.2	457	17 US-09-377-452-4
13	622	27.2	457	17 US-09-377-475-4
14	565	24.7	355	12 US-08-834-033A-6
15	565	24.7	355	13 US-08-956-985-7

16	565	24.7	355	13	US-08-956-985A-7	Sequence 7, Appli
17	565	24.7	355	17	US-09-363-526-5	Sequence 5, Appli
18	565	24.7	355	17	US-09-363-574-5	Sequence 5, Appli
19	498.5	21.8	458	15	US-09-116-639-5	Sequence 5, Appli
20	461	20.2	452	13	US-08-934-254-27	Sequence 27, Appli
21	443.5	19.4	445	14	US-09-048-888-1	Sequence 1, Appli
22	437.5	19.2	448	19	US-60-110-784-5	Sequence 5, Appli
23	433.5	19.0	448	13	US-08-934-254-5	Sequence 5, Appli
24	430.5	18.9	446	12	US-08-834-033A-15	Sequence 15, Appli
25	430.5	18.9	446	13	US-08-956-985-16	Sequence 16, Appli
26	430.5	18.9	446	13	US-08-956-985A-16	Sequence 16, Appli
27	430.5	18.9	446	17	US-09-377-452-5	Sequence 5, Appli
28	430.5	18.9	446	17	US-09-377-475-5	Sequence 5, Appli
29	430	18.8	444	14	US-09-048-888-3	Sequence 3, Appli
30	422	18.5	444	15	US-09-116-639-1	Sequence 1, Appli
31	416	18.2	444	17	US-09-351-525-8	Sequence 8, Appli
32	356	15.6	393	19	US-60-110-784-4	Sequence 4, Appli
33	302.5	13.3	286	19	US-60-110-784-9	Sequence 9, Appli
34	277.5	12.2	252	12	US-08-834-033A-8	Sequence 8, Appli
35	277.5	12.2	252	13	US-08-956-985-9	Sequence 9, Appli
36	277.5	12.2	252	13	US-08-956-985A-9	Sequence 9, Appli
37	277.5	12.2	252	17	US-09-363-526-7	Sequence 7, Appli
38	277.5	12.2	252	17	US-09-363-574-7	Sequence 7, Appli
39	249.5	10.9	446	12	US-08-834-033A-5	Sequence 5, Appli
40	249.5	10.9	446	13	US-08-956-985-6	Sequence 6, Appli
41	249.5	10.9	446	13	US-08-956-985A-6	Sequence 6, Appli
42	249.5	10.9	446	14	US-09-087-578-2	Sequence 2, Appli
43	249.5	10.9	446	15	US-09-145-828-23	Sequence 23, Appli
44	249.5	10.9	446	17	US-09-351-525-2	Sequence 2, Appli
45	249.5	10.9	446	17	US-09-377-452-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
PCT-US99-28655-4
; Sequence 4, Application PC/TUS9928655
; GENERAL INFORMATION:
; APPLICANT: Browne, John et al.
; TITLE OF INVENTION: Desaturases and Methods of Using Them for Synthesis of
; TITLE OF INVENTION: Polyunsaturated Fatty Acids
; FILE REFERENCE: 53860
; CURRENT APPLICATION NUMBER: PCT/US99/28655
; CURRENT FILING DATE: 1999-12-06
; EARLIER APPLICATION NUMBER: 60/111,301
; EARLIER FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Euglena gracilis
PCT-US99-28655-4

Query Match	100.0%	Score 2283;	DB 1;	Length 422;
Best Local Similarity	100.0%	Pred. No. 4.7e-236;		
Matches 422;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKSKRQALSPQLMEQTYDVSAWNPHPGGAETIENYQGRDATDAFVMHFOAFDKLR	60	
Db	1	MKSKRQALSPQLMEQTYDVSAWNPHPGGAETIENYQGRDATDAFVMHFOAFDKLR	60	
QY	61	MPKINSFELPPQAAVNEAQEDFRKLRLELIATGMEDASPLWYSYKISTTLGLGVLGYEL	120	
Db	61	MPKINSFELPPQAAVNEAQEDFRKLRLELIATGMEDASPLWYSYKISTTLGLGVLGYEL	120	
QY	121	MVOYQMYFICAVLLGHYQMGWLSHDICHQHTFKNRNNNNLVGLVFGNGLQGFSVTCWK	180	
Db	121	MVOYQMYFICAVLLGHYQMGWLSHDICHQHTFKNRNNNNLVGLVFGNGLQGFSVTCWK	180	
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Db 229 PEVLIGASVTYMT-----YGIWVCTIFMLAHVLESTEFLLPDGESGAIDDEWAICQIRTT 283

Db 405 LAIKNTCEYKVPY 419

RESULT 9
US-08-307-382-2
: Sequence 2, Application US/08307382
: Patent No. 5552306
: GENERAL INFORMATION:
: APPLICANT: Thomas, Terry L.
: APPLICANT: Reddy, Avutu S.
: APPLICANT: Nuccio, Michael
: APPLICANT: Freyssinet, Georges L.
: TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
: ACID BY A DELTA 6-DESATURASE
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Scully, Scott, Murphy & Presser
: STREET: 400 Garden City Plaza
: CITY: Garden City
: STATE: New York
: COUNTRY: United States
: ZIP: 11530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/307,382
: FILING DATE: 14-SEP-1994
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/817,919
: FILING DATE: 08-JAN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: McNulty, William E.
: REGISTRATION NUMBER: 22,606
: REFERENCE/DOCKET NUMBER: 8383z
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (516) 742-4343
: TELEFAX: (516) 742-4366
: TELEX: 230 901 SANS UR
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 359 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-307-382-2

Query Match 10.5%; Score 239; DB 1; Length 359;
Best Local Similarity 24.9%; Pred. No. 6.5e-20;
Matches 73; Conservative 58; Mismatches 126; Indels 36; Gaps 13;
QY 119 FLMVQYQMFYFVAVLGMHYQMGW-LSDICHQHTFKRNNWNLVGLVFGNGLQGFVSVT 177
Db 60 FAPVIFPVLLGCMVLAIAALAAFSFNVGHDANHNAYSSNPHINRVLGMTY--DFVGLSSF 117
QY 178 CWKDRHN-AHHSATNVQGHDPDIDNLPPLAWSDDVDTRASPIRSK--LIQFOQYFVLV 234
Db 118 LMRYRNYLHHTYTNILGHVDEHG-----DGAVRMSPEQEHVGIYRFQOYFVGLY 169
QY 235 ILLRFTW-CFOCVLTVRSKDRDNQF--YRSQYKKEAIGLALHTLKAFLH-----FFM 286
Db 170 LEIPFYWFLYDVVLNKGKHYHDHKKIPPOPLELASLLGKLLW-LGYVFGPLALGFSI 228
QY 287 PSILTSLVFFVSELVGGFGIAI-VVFMNHYPLEKIGDPWDGCHG-----FVSGQIHET 339
Db 229 PEVLIGASTYMT-----YGVVCTIFMLAHVLESTFTLPDGESGAIDDEWAICQIRT 283
QY 340 MNI-RRGIITDWFGLNQLIEHHLWPTLPRHNLTAVSQVEQLCKQHNLPYR 391

Db 284 ANFATNPNFNNWFCGLNHQVTHLFPNICHYPOLENIINDVCOEFGVEYK 336
RESULT 10
US-08-366-779-2
: Sequence 2, Application US/08366779
: Patent No. 5614393
: GENERAL INFORMATION:
: APPLICANT: Thomas, Terry L.
: APPLICANT: Reddy, Avutu S.
: APPLICANT: Nuccio, Michael
: APPLICANT: Freyssinet, Georges L.
: APPLICANT: Nuders, Andrew N.
: TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
: DELTA 6-DESATURASE
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Scully, Scott, Murphy & Presser
: STREET: 400 Garden City Plaza
: CITY: Garden City
: STATE: New York
: COUNTRY: United States
: ZIP: 11530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/366,779
: FILING DATE: 30-DEC-1994
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Presser, Leopold
: REGISTRATION NUMBER: 19,827
: REFERENCE/DOCKET NUMBER: 8383ZYXW
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (516) 742-4343
: TELEFAX: (516) 742-4366
: TELEX: 230 901 SANS UR
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 359 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-366-779-2

Query Match 10.5%; Score 239; DB 1; Length 359;
Best Local Similarity 24.9%; Pred. No. 6.5e-20;
Matches 73; Conservative 58; Mismatches 126; Indels 36; Gaps 13;
QY 119 FLMVQYQMFYFVAVLGMHYQMGW-LSDICHQHTFKRNNWNLVGLVFGNGLQGFVSVT 177
Db 60 FAPVIFPVLLGCMVLAIAALAAFSFNVGHDANHNAYSSNPHINRVLGMTY--DFVGLSSF 117
QY 178 CWKDRHN-AHHSATNVQGHDPDIDNLPPLAWSDDVDTRASPIRSK--LIQFOQYFVLV 234
Db 118 LMRYRNYLHHTYTNILGHVDEHG-----DGAVRMSPEQEHVGIYRFQOYFVGLY 169
QY 235 ILLRFTW-CFOCVLTVRSKDRDNQF--YRSQYKKEAIGLALHTLKAFLH-----FFM 286
Db 170 LEIPFYWFLYDVVLNKGKHYHDHKKIPPOPLELASLLGKLLW-LGYVFGPLALGFSI 228
QY 287 PSILTSLVFFVSELVGGFGIAI-VVFMNHYPLEKIGDPWDGCHG-----FVSGQIHET 339
Db 229 PEVLIGASTYMT-----YGVVCTIFMLAHVLESTFTLPDGESGAIDDEWAICQIRT 283
QY 340 MNI-RRGIITDWFGLNQLIEHHLWPTLPRHNLTAVSQVEQLCKQHNLPYR 391
Db 284 ANFATNPNFNNWFCGLNHQVTHLFPNICHYPOLENIINDVCOEFGVEYK 336

APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-7

Query Match 12.2%; Score 277.5; DB 2; Length 252;
Best Local Similarity 29.3%; Pred. No. 1e-24;
Matches 80; Conservative 39; Mismatches 105; Indels 49; Gaps 10;
QY 114 GVLGYFLWQYQYFICAVLLGHYQMGWLSHDICHQTFKKNWNLVGLVFGNGLOG 173
DB 5 GVLACTSVFAHQ---IAAALLGLWIOSAYIGHDSGHYVMSKSYNRFQALLSGNCLTG 61
QY 174 FSVTCWKDRNNAHSATNVQGHDPDIDNLPPLAWSE-----DDVTRASPIRKL 222
DB 62 ISIAWKWTINAHNLACSLDYPDLQHIPVFAVSTKFFSLTSRFDYDRKLTGCPVAREL 121
QY 223 IQFOQY-YFLVICI--LLRFIWCQCVLTVRSLKDRDNQYRSQYKKEAIGLALHWTKA 279
DB 122 VSYQHTYYPVNCFGRLNFIQTFLFLSKREVPDRALNE-----AGILVFETWFP 172
QY 280 LF-----HLFFMPSILTSLLVFFVSELVGGFGIAIVFMNHYPLE-KIGDPVNDGH 329
DB 173 LLVSLPLNMPERFFF---VFTSFVTALQH-----IOFTLNHFAADVVGPPPT--GS 219
QY 330 GFSVGOIHETMNIIRRGIIITDFFGGLNVOIEHH 362
DB 220 DWFEKQAAGTIDISCRSYMDWFFGGLQFQLEHH 252

RESULT 8

US-08-833-610-2
Sequence 2, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-2

Query Match 10.9%; Score 249.5; DB 2; Length 446;
Best Local Similarity 24.1%; Pred. No. 5.2e-21;
Matches 105; Conservative 68; Mismatches 167; Indels 95; Gaps 22;
QY 11 LQLEQTYDYSAWYFHPGGAETIENYQGRDATDAFVMVHFOEAFDKLRMPKINP--SF 68
DB 25 LATRGVYDYTKLSRHPGGVDLLLCAGRDVTPVFEXYHAFGADAIMKYYVGTLSN 84
QY 69 ELP--POAAVNEAQEPRKLEELIATGMF-----DASPLWYSYKISTTLGLGVLY 118
DB 85 ELPIPEPTV-----FHKTIKTRV-EGYFTDRNIDPKNRPEIWMGRYAL-----IFGS 130
QY 119 FLWVQIOMYIG-----AVLLGHYQMGWLS-HDICHQTFKKNWNLVGL 165
DB 131 LIASYYAQLEVPFVVERTWLVQVFAITMGFACQVGLNPLHDASHFSVTHNPTVKILGA 190
QY 166 V--FGNGLOQFSVTCWKDRHN-AHHSATNVQGHDPDIDNLPPLAWSDDVTRASPIRKL 222
DB 191 THOFFNCA---SYLVWYQHMGLHHPYNTIAGADPDVST-----SEPDVRIIRPNQWF 241
QY 223 I-OFOQYFVLVICI--LLRFIWCQCVLTVRSLKDRDNQYRSQYKKEAIGL-----A 272
DB 242 VNHQNHMFVFLYGLLAFKVRIOQINILYFVKIND-----AIRVNPISWTWHTV 290
QY 273 LHWTALKALF-----HLFFMPSILTSLLVFFVSELVGGFGIAIVFMNHYPLEKIGDPV 325
DB 291 MFWGGAFFVYRLLVPLQYLP-LGKVLLEFTVADMYSSYVWLTFOANH-VVEVQWPL 348
QY 326 WDGHG-----FSVGOIHETMNIIRRG-----IITDFFGGLNVOIEHHLWPTLPHNLTAV 375
DB 349 PDENGIIQKDWAAQVETTDQYAHDSLHTSIT-----GSLNYQAVHLLFPNVSQHHPI 404
QY 376 SYQVEQLCQKHNLPI 390

TELEFAX: (650) 328-4477
 TELETYPE: N/A
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 355 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-5

Query Match 24.7%; Score 565; DB 2; Length 355;
 Best Local Similarity 34.9%; Pred. No. 1.3e-58;
 Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;

QY 82 DFRKRLREELIATGMDASPLWYSKISTITGLGLVGLVLMVQYQM-----YFIGAVLLGM 136
 DB 1 EVKRLTLFOSLGYDSSKAYAFKVSFNLICWGLSTVIIVAKWGQSTLANVLNLSAALLGL 60
 QY 137 HYQOMGWLSDICHQHFKNRNNNVLGLVFGNGLOGFSVTCWKDRHNAHHSATNVQGH 196
 DB 61 FWOQCGWLHDFLHQVQDFRFGDLFGALGGVCGQFSSSSWKDKHNTHTAAFPNVHGED 120
 QY 197 PDIDNLPPLAWSDDVTRASPI-----SRKLIQFQYIFLVICILLRFLNCFQCVL 247
 DB 121 PDIDTHTPLTWSHALEMFSVDPDELTRMWSREWLNTQWTFPILSFARLSWCLQSIL 180
 QY 248 TVSLKDRDNQFYSQYKK-----EALGLAHLHTLALFLHFLFMPSTLTLVFFVSEL 301
 DB 181 FVLPL-----NGCAHKPGARVPSISLEQLSLAMHTWYLAFLFKDPVNNLVFLVSQA 236
 QY 302 VGGFGIAIVFMNHYPLEKIGDPVWDGHSVGOIHETMNRIRGIIIDWFEGGLNYQIEH 361
 DB 237 VGNLLAIVFSLNHNHNPVTSKEAVDMDFTKQIITGRDVHPLGFANWFTGGLNYQIEH 296
 QY 362 HLMPTLPHRLNLTAVSYQVQLCQKHNLPYRNPPLPHEGLVILLRLVAFARMAEQPA--- 419
 DB 297 HLPSPMRHNFESKIQPAVETLCKKYNRYHTTGMEGTA-----EVSRLNEYSKAASK 350
 QY 419 -GKA 421
 DB 351 MGKA 354

RESULT 4
 US-08-366-779-5
 Sequence 5, Application US/08366779
 Patent No. 5614393
 GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
 APPLICANT: Reddy, Avutu S.
 APPLICANT: Nuccio, Michael
 APPLICANT: Freyssonet, Georges L.
 APPLICANT: Numburg, Andrew N.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,779
 FILING DATE: 30-DEC-1994

CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 8383ZYXW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-366-779-5

Query Match 19.0%; Score 433.5; DB 1; Length 448;
 Best Local Similarity 29.8%; Pred. No. 7.6e-43;
 Matches 121; Conservative 67; Mismatches 167; Indels 51; Gaps 14;

QY 11 LQLMQETDYSAWYNFHPGGAIEIENYQGRDATDAFVMVHFQEAFLKRMKPINPSPEL 70
 DB 25 ISIQKAYDSWVKDHPGGSFPLKSLAGQEVTDFAVAFHPASTW---KNLDKFTTGYL 81
 QY 71 PQAANVEADEDFKREELIATGMDA-----SPLWYSKISTITGLGLVGLVLMVQY 124
 DB 82 -KDYSEVSKDYKRLKVFESKMGLYDKGHIMEFATLCF---IAMLFAMSYGVLFCEGV 137
 QY 125 QMFIAGVALLGMHQWGLSHDICHQTFKNRNNNVLGLVFGNGLOGFSVTCWKDRHN 184
 DB 138 LVHLSFCGLGFLQISQWIGHAGHYVVSLSRLNFMGIFAANCUSGISGIGWKNHN 197
 QY 185 AHSATNVQGHDPIDNLPPLAWS-----EDVTRASPIRKLQFOQYFELV 232
 DB 198 AHTACSLNLEVDPLQIPLVWSSKFFGSLTSHEKRLTFDS-LSRFFVSYQHTFVP 256
 QY 233 ICILLRIFWQCVLTVRSKDRDNQFYSQYKKEATGLAHLHTLALFLHFLFHPSPILTS 292
 DB 257 IMCAARLNMVQSLI---MLLTNRNVSRAQ---ELLGC-----LVFSIWY--PLVLS 301
 QY 293 LL-----VFFVSELVGGFGIAIVF--MNHYPLE-KIGDPVWDGHSVGOIHETMNR 344
 DB 302 CLPNWGERIMFVIASLSVTGMQVQFSLNHFSSSVYVQKP--KGNWFEKOTDGLDSC 359
 QY 345 GIITDWFEGGLNYQIEHHLWPTLPHRLNLTAVSYQVQLCQKHNLPY 390
 DB 360 PPMWDFHGGSQFQIEHHLFPMKPRCNRKISPYVIELCKKHNLPY 405

RESULT 5
 US-08-789-936-5
 Sequence 5, Application US/08789936
 Patent No. 5789220
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 APPLICANT: Reddy, Avutu S.
 APPLICANT: Nuccio, Michael
 APPLICANT: Freyssonet, Georges L.
 APPLICANT: Numburg, Andrew N.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

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Db 81 -----ANFYV---GDIDESDRDIKNDDFAAEVRKRLTLFQSLGYDSSKAYIAFKVSFN 131
Qy 111 LGLGVLGYFLMVQYQM-----YFICAVLLGMHYQOMGLSHDICHQHTFKNNWNLVGL 165
Db 132 LCINGLSTVIIVAKWGQTSTLANVLSAALLGLFWQCGWLAHDFLHHQVQDFRFGDLFGA 191
Qy 166 VFGNLOGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDDVTRASPI-----219
Db 192 FLGGVCGQFSSSWKDKHNTHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVDEELTR 251
Qy 219 --SRKLIQOQYFYFLVICILLRFIWCFCQVLTVRSLKDRDNQFYRSQYKK-----EAG 270
Db 252 MWSRFMVLNQTWFYFPIILSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
Qy 271 LALHWTALKALHFLFMPISILSLVFFVSELVGGFIAIVFMNHYPLEKIGDPVWDGSHG 330
Db 308 LAMHWTWYLATMFLFIKDPVNMVLYFLVSVQVGNLLAIVFSLNHNMPVSKESAEVMD 367
Qy 331 FSVQIHTMNRIRGIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVEQLCKKHNLPLY 390
Db 368 FFTQIITGRDVHPGLFANWFTGGLNYQIEHHLFSPMRHNFPSKIOPAVETLCKKYNRY 427
Qy 391 RNPLPHEGLVILLRYLAVFARMAEKQPA-----GKA 421
Db 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

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RESULT 2

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US-08-833-610-4
; Sequence 4, Application US/08833610
; Patent No. 5972664
; GENERAL INFORMATION:
; APPLICANT: KNUITZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,610
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.123.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)328-4400
; TELEFAX: (650)328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-833-610-4

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Query Match 27.2%; Score 622; DB 2; Length 457;
Best Local Similarity 32.7%; Pred. No. 3.3e-65;
Matches 149; Conservative 76; Mismatches 174; Indels 56; Gaps 11;

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Qy 2 KSKROALSPLOLM--EQYDVSAWVNFHPGGAIEITENQGRDATDAFVMVHFOEAFDKLK 59
Db 23 EGKDAEAPFLMIIDNKYVDYREFVPDHPGGS-VILTHVGDKGTVDFTFPEAAWETL- 81
Qy 60 RMPKINPSEFLPPOAAVNEAQEDF-----RKLREELIATGMFEDASPLWYSYKISTT 110
Db 81 -----ANFYV---GDIDESDRDIKNDDFAAEVRKRLTLFQSLGYDSSKAYIAFKVSFN 131
Qy 111 LGLGVLGYFLMVQYQM-----YFICAVLLGMHYQOMGLSHDICHQHTFKNNWNLVGL 165
Db 132 LCINGLSTVIIVAKWGQTSTLANVLSAALLGLFWQCGWLAHDFLHHQVQDFRFGDLFGA 191
Qy 166 VFGNLOGFSVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDDVTRASPI-----219
Db 192 FLGGVCGQFSSSWKDKHNTHAAPNVHVEDPDIDTHPLLTWSEHALEMFSDVDEELTR 251
Qy 219 --SRKLIQOQYFYFLVICILLRFIWCFCQVLTVRSLKDRDNQFYRSQYKK-----EAG 270
Db 252 MWSRFMVLNQTWFYFPIILSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
Qy 271 LALHWTALKALHFLFMPISILSLVFFVSELVGGFIAIVFMNHYPLEKIGDPVWDGSHG 330
Db 308 LAMHWTWYLATMFLFIKDPVNMVLYFLVSVQVGNLLAIVFSLNHNMPVSKESAEVMD 367
Qy 331 FSVQIHTMNRIRGIITDWFEGGLNYQIEHHLWPTLPRHNLTAVSQVEQLCKKHNLPLY 390
Db 368 FFTQIITGRDVHPGLFANWFTGGLNYQIEHHLFSPMRHNFPSKIOPAVETLCKKYNRY 427
Qy 391 RNPLPHEGLVILLRYLAVFARMAEKQPA-----GKA 421
Db 428 HTTGMIEGTA-----EVFSRLNEVSKAASKMGKA 456

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RESULT 3

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US-08-834-655-5
; Sequence 5, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUITZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400

```


[illegible]

Search completed: February 25, 2000, 04:45:48
Job time: 23783 sec

QY 298 VSELYGGGIAIVFNNHYPLEKIGDPVMDGHGFSVQIHTMNRIRGIIITDFFGGLNY 357
 DB 175 FIRELESHFVWVQTNHIVMEIDQAYRD--WFS-SQLTATCNVQSFDFWFSGLNLF 231
 QY 358 QIEHHLWPTLPRNLTAVSYQVQLCOKNLPYRNPLPHEGLVILLRYL 406
 DB 232 QIEHHLFPTMPRNLHKLAPLVKSLCAKHGIEYQERKPLLRALLDIIRSL 280

RESULT 14
 W95513
 ID W95513 standard; Protein: 615 AA.
 AC W95513;
 DE 26-MAR-1999 (first entry)
 DT Amino acid sequence of human desaturase gene contig 2535.
 KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW Polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW Stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 295 /note= "encoded by TGA"
 FT Misc_difference 321 /note= "encoded by TGA"
 FT Misc_difference 458 /note= "encoded by TGA"
 FT Misc_difference 491 /note= "encoded by TAA"
 FT Misc_difference 517 /note= "encoded by TAG"
 FT Misc_difference 535 /note= "encoded by TGA"
 FT Misc_difference 550 /note= "encoded by TGA"
 FT Misc_difference 615 /note= "encoded by TG"
 PN W09846764-A1.
 PD 22-OCT-1998.
 PE 10-APR-1998; U07421.
 PR 24-OCT-1997; US-956985.
 PR 11-APR-1997; US-833610.
 PR 11-APR-1997; US-834033.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 PI WPI: 99-080739/07.
 DR N-PSDB; X00909.
 PT Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 PS Claim 48; Page 167-169; 210pp; English.
 CC The invention relates to a nucleic acid construct that contains at least
 CC one of the nucleotide sequences (X00889 to X00891) encoding Mortierella
 CC alpina delta 6, delta 12 and delta 5 desaturases (W95504 to W95506)
 CC respectively, coupled to an expression control sequence functional in
 CC plants. Recombinant plant cells containing at least one DNA encoding a
 CC M. alpina fatty acid desaturase (FAD), can be used for the production of
 CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants
 CC containing them are used to produce oils such as linoleic acid,
 CC arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid,
 CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
 CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and

CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
 CC related coding sequences. Recombinant plants can produce high yields of
 CC PUFA, since new pathways can be created and unwanted ones suppressed.
 CC Plants can be engineered to express oils of particular PUFA composition,
 CC e.g. one similar to that in human milk, and product recovery is simpler
 CC than with e.g. fish. Sequences W95508-514 represent amino acid sequences
 CC of various contigs of human desaturase genes which are similar to the
 CC M. alpina desaturase sequences.
 SQ Sequence 615 AA;

Query Match 13.6%; Score 310; DB 1; Length 615;
 Best Local Similarity 29.4%; Pred. No. 1.1e-27;
 Matches 85; Conservative 46; Mismatches 126; Indels 32; Gaps 8;
 QY 129 IGAVLGMHYQQMGWLSHDICHTKFNWNNLVGLFNGLOGFSVTCWKDRHNAHS 189
 DB 13 ITAFVLATSOAQAGLQHDYGVHLSVYRKPKWNHVKFVIGHLKGASANNWNRHFQHA 72
 QY 189 ATNVOGHDPDIDMLPLANSEDDVTRSPI--SRKLIQF-----QQYYFLV-ICILLRF 239
 DB 73 KPNIFKDPDVMNLMHVFVLGE-----WQPIEYCKKLLKLYPNHQHEYFFLGGPLLP 127
 QY 240 IMCFQCVLTVRSLKDRDNQFYRSQYKKAIGLALHWTALFHLFFMP--SILTSLVFF 297
 DB 128 YFOYQIIMT-----IVHKNVVDLAWAVSYIRFTYIPFYGILGALLFLN 174
 QY 298 VSELVGGFGIAIVFNNHYPLEKIGDPVMDGHGFSVQIHTMNRIRGIIITDFFGGLNY 357
 DB 175 FIRELESHFVWVQTNHIVMEIDQAYRD--WFS-SQLTATCNVQSFDFWFSGLNLF 231
 QY 358 QIEHHLWPTLPRNLTAVSYQVQLCOKNLPYRNPLPHEGLVILLRYL 406
 DB 232 QIEHHLFPTMPRNLHKLAPLVKSLCAKHGIEYQERKPLLRALLDIIRSL 280

RESULT 15
 W84141
 ID W84141 standard; Peptide: 252 AA.
 AC W84141;
 DT 15-FEB-1999 (first entry)
 DE Desaturase enzyme peptide sequence.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846763-A1.
 PD 22-OCT-1998.
 PE 10-APR-1998; U07126.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 PI WPI: 98-594582/50.
 DR New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed
 PS Example 2; Pages 103-104; 165pp; English.
 CC The present sequence represents a peptide derived from a desaturase
 CC enzyme. The specification describes methods for desaturating a
 CC fatty acid and for producing a desaturated fatty acid by expressing
 CC increased levels of a desaturase. Desaturases can be used for
 CC desaturating fatty acids. The enzymes can be used to produce
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
 CC cancer, diabetes or eczema or reduce blood pressure. They can also be
 CC used to inhibit platelet aggregation, cause vasodilation, lower

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Db 416 RSL 418

RESULT 12
ID W84155
AC W84155:
DE Human desaturase enzyme encoded by contig 2535.
KW Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome; human;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 608 /note= "not specified"
PD W09846763-A1.
PN 22-OCT-1998.
PF 10-APR-1998; U07126.
PR 11-APR-1997; US-834655.
PA (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
PI WPI; 98-594582/50.
DR N-PSDB; V63642.
PT New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
PS Example 12; Pages 123-124; 163pp; English.
CC The present sequence is a human desaturase enzyme. The cDNA sequence was
CC identified based on homology between human cDNA sequences and Mortierella
CC alpina desaturase gene sequences. The specification describes methods for
CC desaturating a fatty acid and for producing a desaturated fatty acid by
CC expressing increased levels of a desaturase. The enzyme can be used for
CC desaturating fatty acids. The enzyme can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma,
CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
CC can also be used to inhibit platelet aggregation, cause vasodilation,
CC lower cholesterol levels, inhibit proliferation of vessel wall smooth
CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
CC and other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat
CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
SQ Sequence 608 AA;

Query Match 13.6%; Score 310; DB 1; Length 608;
Best Local Similarity 29.4%; Pred. No. 1.1e-27;
Matches 8; Conservative 46; Mismatches 126; Indels 32; Gaps 8;

QY 129 IGAVLLGHVYQMGWLSHDICHHTFKNRNWNNLVGLVFGNGLOGFSVTCWKDRHNAHNS 188
DB 13 ITAFVLATSAQAQAGWLQHDYGLSVYRKPNWHLVHKVIGHLKGASANNWNRHFQHA 72

QY 189 ATNVQGHDPDIDNLPPLAWSEDDVTRASPI--SRKLQF-----QQYFLV-ICILLRF 239
DB 73 KPNIFHKDPDYNMLHFVFLGE-----WQPIEYGGKKLKLPLYNHQHVEFFLGPPLIPM 127

QY 240 IWCFOCVLTVRSKDRDNQFYSQYKKEAIGLALHTLWTKALFLHFFMP--SILTSLLVFF 297
DB 128 YFQIQITMTM-----IVHKNWDLAWAVSYIIRFFITYIPFYIGLALLFLN 174

QY 298 VSELVGGFGIAIVFMNHPLEKIGDPVMDGHSVGQIHETMTNRRGIITDWEFFGLNY 357
DB 128 YFQIQITMTM-----IVHKNWDLAWAVSYIIRFFITYIPFYIGLALLFLN 174

Db 175 FIRELESHWFVWVTQMNHYVMEIQDEAYRD--WFS-SOLTATCNVEQSFNDWFESGLNF 231

QY 358 QIEHHLNPTLPRHNLTAVSQVEQLCKQKHNLPYRNPLPHEGLVILLRYL 406
DB 232 QIEHHLFTMPRHNHLKIAPLVKSLCAKHKIEYQEKPLRLALLDIRSL 280

RESULT 13
ID W85134
AC W85134:
DE 11-FEB-1999 (first entry)
DE A desaturase enzyme encoded by contig 2535.
KW Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome; human;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 608 /note= "not specified"
PD W09846765-A1.
PN 22-OCT-1998.
PF 10-APR-1998; U07422.
PR 11-APR-1997; US-833610.
PA (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
PI WPI; 99-009334/01.
DR N-PSDB; V82641.
PT New nucleic acid encoding delta5 and other desaturase enzymes -
PT useful in production of oils of increased arachidonic acid content,
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
PT Claim 87; Pages 117-119; 153pp; English.
CC The present sequence represents a human desaturase enzyme. The enzyme
CC sequence is used in the methods of the invention. The specification
CC describes methods for desaturating a fatty acid and for producing a
CC desaturated fatty acid by expressing increased levels of a desaturase.
CC The enzyme can be used for desaturating fatty acids. The enzyme can be
CC used to produce polyunsaturated fatty acids, which can be used for
CC treating malnutrition, in pharmaceutical compositions, in cosmetics or
CC in animal feed. The polyunsaturated fatty acids can be used for treating
CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
CC They can also be used to inhibit platelet aggregation, cause
CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
CC wall smooth muscle and fibrous tissue, reduce or prevent
CC gastro-intestinal bleeding and other side effects caused by non-steroidal
CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after
CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
CC syndrome, hypertension and inflammatory skin disorders.
SQ Sequence 608 AA;

Query Match 13.6%; Score 310; DB 1; Length 608;
Best Local Similarity 29.4%; Pred. No. 1.1e-27;
Matches 8; Conservative 46; Mismatches 126; Indels 32; Gaps 8;

QY 129 IGAVLLGHVYQMGWLSHDICHHTFKNRNWNNLVGLVFGNGLOGFSVTCWKDRHNAHNS 188
DB 13 ITAFVLATSAQAQAGWLQHDYGLSVYRKPNWHLVHKVIGHLKGASANNWNRHFQHA 72

QY 189 ATNVQGHDPDIDNLPPLAWSEDDVTRASPI--SRKLQF-----QQYFLV-ICILLRF 239
DB 73 KPNIFHKDPDYNMLHFVFLGE-----WQPIEYGGKKLKLPLYNHQHVEFFLGPPLIPM 127

QY 240 IWCFOCVLTVRSKDRDNQFYSQYKKEAIGLALHTLWTKALFLHFFMP--SILTSLLVFF 297
DB 128 YFQIQITMTM-----IVHKNWDLAWAVSYIIRFFITYIPFYIGLALLFLN 174

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Db 302 CLPNWGERIMFVIAISLVTGQQVQFSLNHFFSSSVYVVKP--KGNWNFEKOTDGTDLDISC 359
QY 345 GIITDFFGGLNQIEHHLNPTLPRNLTAVSQVEOLCKHNLPLY 390
Db 360 PWNWDFHGLQFOIEHHLFPRKPRCNLRKISPYVIELCKHNLPLY 405

RESULT 9
W84156
ID W84156 standard; Protein: 746 AA.
AC W84156;
DE Human desaturase enzyme encoded by contig 253538a.
KW Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome; human;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Homo sapiens.
EH Key
FT Misc_difference 746
FT /note= "not specified"
PN W09846763-A1.
PD 22-OCT-1998.
PR 10-APR-1998: U07126.
PR 11-APR-1997: US-834655.
PA (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
DR WPI: 98-594582/50.
DR N-PSDB: V63643.
PT New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
PS Example 12; Pages 124-126; 165pp; English.
CC The present sequence is a human desaturase enzyme. The cDNA sequence was
CC identified based on homology between human cDNA sequences and Mortierella
CC alpina desaturase gene sequences. The specification describes methods for
CC desaturating a fatty acid and for producing a desaturated fatty acid by
CC expressing increased levels of a desaturase. The enzyme can be used for
CC desaturating fatty acids. The enzyme can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma,
CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
CC can also be used to inhibit platelet aggregation, cause vasodilation,
CC lower cholesterol levels, inhibit proliferation of vessel wall smooth
CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
CC and other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat
CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
CC Sequence 746 AA;

Query Match 18.5%; Score 421.5; DB 1; Length 746;
Best Local Similarity 28.1%; Pred. No. 1e-40;
Matches 119; Conservative 72; Mismatches 177; Indels 55; Gaps 13;

QY 11 LQLEMTQYDVSANVNFHGGAEIENYQGRDADFAMVWHFQEDFK-----LKRMPK 63
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 24 LVIDRKVYNSEFTRHFGGSGVISHYAGQDADFVAFHKNGLVKYKMYNMLLIGELSP 83
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 64 INPSFELPPQAAVNEAQEDFKRLRELIATGMDASPLWYSKYI-----STTLGLGV 115
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 84 EQPFE---PTKNKELTDEFRELATVEMGLMKANHFVFLYLHILLDGAANLTLMV 140
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 116 LGYFLMVOYMYFIGAVLLGMHYQ-QMGWLSHDICHQHTFKNRNWNVLVGLVEGNGLOGF 174
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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Db 141 FG-----TSFLPFLLCALLSVLVAQQAAGNLQHDYGHLSVYRKPKNHNLVHKFVIGHLKGA 196
QY 175 SVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDDVTRASPI--SRKLIQF-----Q 226
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 197 SANWNHRHFQHHAKPNIFHKDPDVNKNLHVFLGE-----WQPIEYGGKKLKLPLYNHQH 251
QY 227 QYFLV-ICILLRFIWCFCVLTVRSCLKDRDNDFYRSQYKKEAIGALHWTALKALFHLFF 285
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 252 EYFFLIGPLLPIMFYQYQIIMT-----IVHKNWVDLAWAVSYVIRFFITY 298
QY 286 MP--SILTSLLVFFVSELVGGGCIATVEMNHYPLEKIGDPVWDGHSFGVGOIHETMNR 343
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 299 IPFYGLIGALLFLNFRFLESHFWVWTONNHVIMEDQAYRD--WFS-SQTATCNVE 355
QY 344 RGIITDFFGGLNQYIEHHLNPTLPRNLTAVSQVEOLCKHNLPRNPLPHEGLVILL 403
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 356 QSFENDWFSGHLNFQIEHHLFPTMPRNLHKLAPVKSILCAKHGIEQEKPLLRALLDII 415
QY 404 RVL 406
Db 416 RSL 418

RESULT 10
W85135
ID W85135 standard; Protein: 746 AA.
AC W85135;
DE A desaturase enzyme encoded by contig 253538a.
KW Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Homo sapiens.
EH Key
FT Misc_difference 746
FT /note= "not specified"
PN W09846765-A1.
PD 22-OCT-1998.
PR 10-APR-1998: U07422.
PR 11-APR-1997: US-833610.
PA (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
DR WPI: 99-009334/01.
DR N-PSDB: V82642.
PT New nucleic acid encoding delta5 and other desaturase enzymes -
PT useful in production of oils of increased arachidonic acid content,
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
PS Claim 87; Pages 119-120; 153pp; English.
CC The present sequence represents a human desaturase enzyme. The enzyme
CC sequence is used in the methods of the invention. The specification
CC describes methods for desaturating a fatty acid and for producing a
CC desaturated fatty acid by expressing increased levels of a desaturase.
CC The enzyme can be used for desaturating fatty acids. The enzyme can be
CC used to produce polyunsaturated fatty acids, which can be used for
CC treating malnutrition, in pharmaceutical compositions, in cosmetics or
CC in animal feed. The polyunsaturated fatty acids can be used for treating
CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
CC They can also be used to inhibit platelet aggregation, cause
CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
CC wall smooth muscle and fibrous tissue, reduce or prevent
CC gastro-intestinal bleeding and other side effects caused by non-steroidal
CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after
CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
CC syndrome, hypertension and inflammatory skin disorders.
CC Sequence 746 AA;

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KW chilling resistance; oilseed.
 OS Borago officinalis.
 FH Key Location/Qualifiers
 FT Region 156..163
 FT /label= Lipid_box
 FT region 196..200
 FT /label= Metal_box-1
 FT region 372..377
 FT /label= Metal_box-2
 PN W09621022-A2.
 PD 11-JUL-1996.
 PF 28-DEC-1995; IB1167.
 PR 30-DEC-1994; US-366779.
 PA (RHON) RHONE POULENC AGROCHIMIE.
 PI Freyssinet GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
 DR WPI: 96-333997/33.
 DR N-PSDB: T30395.
 PT transgenic plants comprising the borage delta-6-desaturase gene
 PT show increased production of gamma linolenic acid and having
 PT increased resistance to chilling
 PS Claim 3: Page 52-53: 75pp; English.
 CC Borage delta-6-desaturase (R98455) catalyses the conversion of
 CC linoleic acid to gamma-linolenic acid (GLA). Its sequence was
 CC deduced from that of the delta-6-desaturase gene (T30395) isolated
 CC from a borage membrane-bound polysomal library. The sequence is
 CC distinct from that of Synecocystis delta-6-desaturase (R98456).
 CC Expression of the desaturase in transgenic plants, esp. sunflower,
 CC soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
 CC increased GLA prodn. Alteration of the plant membrane lipids as a
 CC result of expression of the desaturase may also result in increased
 CC resistance to chilling.
 SQ Sequence 448 AA;

Query Match 19.3%; Score 439.5; DB 1; Length 448;
 Best Local Similarity 30.0%; Pred. No. 3.6e-43;
 Matches 122; Conservative 67; Mismatches 166; Indels 51; Gaps 14;

QY 11 LQMLEQTVDSVSNWVNFHFGGAEIENYOGRDATDAFVWVHFQAEADKLRMPKINPSPEL 70
 DB 25 ISIQKAYDVSDWVNDHFGGSPPLKSLAGQEVTDFAVAFHASTW---KNLDKFTGYL 81
 QY 71 PQAANVQAQDFRKLREELIATGMFDA-----SPLWYSYKISTTLGLVGLGYFLWVOY 124
 DB 82 -KDSVSEVSKDYRLKLVFEFSKMGLYDKKGIMFATLCF---IAMLFMSVYGVLFCEGV 137
 QY 125 QMYFAGVLLGMHVOQMGLSHDICHQTFNKRNNNNLVGLVFGNGLQGSFVTCWKDRHN 184
 DB 138 LVHLFSGCLMGFLMTQSGWIGHGAGHYMVVSDSLNKFMGIFAANCLSGISIGMKWKNHN 197
 QY 185 AHSATNVQGHDPDIDNLPPLAWS-----EDDVTRASPISRKLIQFOQYYFLV 232
 DB 198 AHTACNSLEYDPLQIYPLVWSKFGSLSHFYERKLTDFS--LSRFFVSYQHWTFYP 256
 QY 233 ICILLRFTWCQCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTLLKALFLHFEMPISILTS 292
 DB 257 IMCAARLNMVQSLI---MLLTKNVSYRAQ---ELLCG-----LVFSWY--PLVVS 301
 QY 293 LL-----VFFVSELVGGFGIAIVF--MNHYPLE-KIGDPVWDGHGFSVGQIHTMNI 344
 DB 302 CLPNWGERIMFVIASLVTGMQVQFSLNHFSSSVYVGP--KGNMFKEKTDGTDLTDISC 359
 QY 345 GIITDWFEGGLNVOIEHLLWPTLRPHNLTAVSQVEQLCKHNL 390
 DB 360 PPWMDWFHGGLOFQIEHLLFPMPRCNLRKISPYVIELCKHNL 405

RESULT 6
 ID W67471
 AC W67471 standard; Protein; 448 AA.
 DT 02-MAR-1999 (first entry)
 DE Borage delta-6 desaturase protein.

KW Upstream region; regulatory region; sunflower; albumin; seed; expression;
 OS Borago officinalis.
 FH Key Location/Qualifiers
 FT Region 40..44
 FT /note= "cytochrome b5 haem-binding motif"
 FT Domain 156..163
 FT /note= "His-rich metal binding motif"
 FT Domain 196..200
 FT /note= "His-rich metal binding motif"
 FT Domain 373..377
 FT /note= "His-rich metal binding motif"
 PN W09845460-A1.
 PD 15-OCT-1998.
 PF 09-APR-1998; U07178.
 PR 09-APR-1997; US-831570.
 PA (RHON) RHONE-POULENC AGROCHIMIE.
 PI Beremand PD, Nunberg AN, Thomas TL;
 DR WPI: 98-583201/49.
 DR N-PSDB: V34398.
 PT New sunflower albumin 5' regulatory region - useful for directing
 PT altered lipid metabolism in plant seeds
 PS Example 2: Fig 1: 38pp; English.
 CC This sequence corresponds to the borage (Borago officinalis) delta-6
 CC desaturase enzyme. The encoding lipid metabolism gene is an example
 CC of a heterologous gene which can be expressed at high levels in a
 CC seed-specific manner in transgenic plants, when placed under control
 CC of the sunflower albumin gene 5' regulatory region (V34397).
 SQ Sequence 448 AA;

Query Match 19.3%; Score 439.5; DB 1; Length 448;
 Best Local Similarity 30.0%; Pred. No. 3.6e-43;
 Matches 122; Conservative 67; Mismatches 166; Indels 51; Gaps 14;

QY 11 LQMLEQTVDSVSNWVNFHFGGAEIENYOGRDATDAFVWVHFQAEADKLRMPKINPSPEL 70
 DB 25 ISIQKAYDVSDWVNDHFGGSPPLKSLAGQEVTDFAVAFHASTW---KNLDKFTGYL 81
 QY 71 PQAANVQAQDFRKLREELIATGMFDA-----SPLWYSYKISTTLGLVGLGYFLWVOY 124
 DB 82 -KDSVSEVSKDYRLKLVFEFSKMGLYDKKGIMFATLCF---IAMLFMSVYGVLFCEGV 137
 QY 125 QMYFAGVLLGMHVOQMGLSHDICHQTFNKRNNNNLVGLVFGNGLQGSFVTCWKDRHN 184
 DB 138 LVHLFSGCLMGFLMTQSGWIGHGAGHYMVVSDSLNKFMGIFAANCLSGISIGMKWKNHN 197
 QY 185 AHSATNVQGHDPDIDNLPPLAWS-----EDDVTRASPISRKLIQFOQYYFLV 232
 DB 198 AHTACNSLEYDPLQIYPLVWSKFGSLSHFYERKLTDFS--LSRFFVSYQHWTFYP 256
 QY 233 ICILLRFTWCQCVLTVRSKDRDNQFVRSQYKKEAIGLALHWTLLKALFLHFEMPISILTS 292
 DB 257 IMCAARLNMVQSLI---MLLTKNVSYRAQ---ELLCG-----LVFSWY--PLVVS 301
 QY 293 LL-----VFFVSELVGGFGIAIVF--MNHYPLE-KIGDPVWDGHGFSVGQIHTMNI 344
 DB 302 CLPNWGERIMFVIASLVTGMQVQFSLNHFSSSVYVGP--KGNMFKEKTDGTDLTDISC 359
 QY 345 GIITDWFEGGLNVOIEHLLWPTLRPHNLTAVSQVEQLCKHNL 390
 DB 360 PPWMDWFHGGLOFQIEHLLFPMPRCNLRKISPYVIELCKHNL 405

RESULT 7
 ID W98130
 AC W98130 standard; Protein; 448 AA.
 DT 21-JUN-1999 (first entry)
 DE Borage delta-6 desaturase.
 KW Delta-6 desaturase; borage; oleosin; AtS21; promoter;
 KW transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
 KW gamma-linolenic acid; octadecatetraenoic acid.

CC for producing a desaturated fatty acid by expressing increased levels of
CC a desaturase. The present desaturase is an enzyme which introduces a
CC double bond carbons 6 and 7 from the carboxyl end of a fatty acid
CC molecule. The enzyme can be used for desaturating fatty acids. The
CC enzyme can be used to produce polyunsaturated fatty acids, which can
CC be used for treating malnutrition, in pharmaceutical compositions,
CC in cosmetics or in animal feed. The polyunsaturated fatty acids can
CC be used for treating e.g. restenosis after angioplasty, inflammation,
CC rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema
CC or reduce blood pressure. They can also be used to inhibit platelet
CC aggregation, cause vasodilation, lower cholesterol levels, inhibit
CC proliferation of vessel wall smooth muscle and fibrous tissue,
CC reduce or prevent gastro-intestinal bleeding and other side effects
CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
CC and chronic fatigue after viral infections, treat AIDS, multiple
CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
CC disorders.
CC Sequence 457 AA;

Query Match 27.2%; Score 622; DB 1; Length 457;
Best Local Similarity 32.7%; Pred. No. 1.1e-64; Indels 56; Gaps 11;
Matches 149; Conservative 76; Mismatches 174;

QY 2 KSKQALSPLOLM--EQYDVSAMVNFHFGGAEIENYQGRDATDAFMVHFQAEFDKILK 59
DB 23 EGKDAEAPFLMIDNKYDREFVDPDHGGS-VILTHVGRDGTVDFTFHEAWEIL- 81
QY 60 RMPKINSPFLPQAAVNEAQEDF-----RKLRDELATGMFDASPLWYSKIYSTT 110
DB 81 -----ANFYV---GDIDESDRDIKNDDFAAEVRKRLTLFQSLGYDSSKAYAFKVSFN 131
QY 111 LGLVGLVFLAVQYQM-----YFICAVLGMHYQMGWLSHDICHQTFKKNRWNVLGL 165
DB 132 LCINGLSVIVAKMGQOTSLANVLVSAALLGFWQCGWLAHDFLHQVQDFRFGDLFGA 191
QY 166 VFGNGQGSFVTCWDRNNAHSAATVQCHDIDNLPPLAWSEDDVTRASPI----- 219
DB 192 FLGGVCGQFSSWWDKNTHAAFPNVHVEDPDIDTHPLLTWSEHALEMFSVDPELTR 251
QY 219 --SRKIQOQYFVLVICILRLFWCFCVLTVRSKDRDNQFYRSQYK-----EAIG 270
DB 252 MWSRFVNLQWTFYPIILSFARLSWCLQSILFVLP-----NGQAHKPSGARVPISLVEQLS 307
QY 271 LALHWTALKALPHLFPMPISLTLVFFVSELVGGFIAIVFMNHYPLEKIGDPVWDG 330
DB 308 LAMHTWYLATMFLFIKDPVNNLVYFLVSQVCGNLLAIVFSLNHNMGMPVISKEEAVDM 367
QY 331 FSVGQIHETMNRRIIITDWFGGLNYQIEHLWPTLPRLNLTAVSYQVQLCQKHNLFPY 390
DB 368 FTFQIITGRDVHGLFANFWTGGNLYQIEHLFSPMPHNFSTKQPAVETILCKYNYRY 427
QY 391 RNPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
DB 428 HTTGMEICTA-----EVFSRLNEVSKAASKMGA 456

RESULT 4
W84139 ID W84139 standard; Peptide; 355 AA.
AC W84139;
DT 15-FEB-1999 (first entry)
DE Desaturase enzyme peptide sequence.
KW Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Unidentified.
PN W09846763-A1.
PD 22-OCT-1998.

PF 10-APR-1998; U07126.
PR 11-APR-1997; US-834655.
PA (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
DR WPI; 98-594502/50.
PT New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
PT Example 2; Pages 101-102; 165pp; English.
PS The present sequence represents a peptide derived from a desaturase
CC enzyme. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. Desaturases can be used for
CC desaturating fatty acids. The enzymes can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
CC cancer, diabetes or eczema or reduce blood pressure. They can also be
CC used to inhibit platelet aggregation, cause vasodilation, lower
CC cholesterol levels, inhibit proliferation of vessel wall smooth muscle
CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
CC other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
CC Sequence 355 AA;

Query Match 24.7%; Score 565; DB 1; Length 355;
Best Local Similarity 34.9%; Pred. No. 3.9e-58;
Matches 127; Conservative 58; Mismatches 145; Indels 34; Gaps 6;

QY 82 DFRKURELIATGMFDASPLWYSKISTLGLVGLVFLAVQYQM-----YFICAVLGLM 136
DB 1 EYVKRLTLFQSLGYDSSKAYAFKVSFNLCIWLSTVIVAKMGQOTSLANVLSAALLGL 60
QY 137 HYQMGWLSHDICHQTFKKNRWNVLVGLVFGNGQGSFVTCWDRNNAHSAATVQCHD 196
DB 61 FQWQCGWLAHDFLHQVQDFRFGDLFGAFLGVCQCGFSSWWDKNTHAAFPNVHGED 120
QY 197 PDIDNLPPLAWSEDDVTRASPI-----SRKIQOQYFVLVICILRLFWCFCVL 247
DB 121 PDIDTHPLLTWSEHALEMFSVDPELTRMWSREYNLTQTFYPTLSFARLSWCLQSIL 180
QY 248 TVRSKDRDNQFYRSQYK-----EATGLALHWTALKALPHLFPMPISLTLVFFVSEL 301
DB 181 FVLP-----NGQAHKPSGARVPISLVEQLSLAMHTWYLATMFLFIKDPVNNLVYFLV 236
QY 302 VGGFIAIVFMNHYPLEKIGDPVWDGHSVQVGHETMNRRIIITDWFGGLNYQIEHL 361
DB 237 VCGNLLAIVFSLNHNMGMPVISKEEAVDMDFTFQIITGRDVHGLFANFWTGGNLYQIEH 296
QY 362 HLWPTLPRLNLTAVSYQVQLCQKHNLFPRLPHEGLVILLRYLAVFARMAEKOPA--- 419
DB 297 HLFPSMPHNFSTKQPAVETILCKYNYRYHTTGMEICTA-----EVFSRLNEVSKAASK 350
QY 419 -GKA 421
DB 351 MGKA 354

RESULT 5
R98455 ID R98455 standard; Protein; 448 AA.
AC R98455;
DT 15-SEP-1996 (first entry)
DE Borage delta-6-desaturase.
KW Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
KW polyunsaturated fatty acid; octadecatetraenoic acid;

QY 111 LGLVGLYFLMVOYOM-----YFIGAVLLGMHYOQMGWLSHDICHOTKNNWNNVLGL 165
 Db 132 LCIWGLSTVIVAKWGOTSTLANVLSAALLGLFWOCCGLAHDFLHHQVQDFRFGWDLFGA 191
 QY 166 VFGNGLOGFVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDEDDVTRASPI----- 219
 Db 192 FLGGVCGGFSWKKHNTTHAAPNVHGEDPDIDTHTPLTWSEHALEMESDVPDEELTR 251
 QY 219 --SRKLIQOQYVFLVICILLRFTWCFCQVLTVRSLKDRDNQFYRSQYK-----BAIG 270
 Db 252 MWSRFVNLQNTWYFPLSFAUSWCLQSILFVLP-----NGQAHKPSGARVPISLVBQLS 307
 QY 271 LALHWTLKALFLHFFMPSILTSLLVFEVSELVGGFIAIVFMNHYPLEKIGDPVWDGHC 330
 Db 308 LAHWHTWYLTATMFLFKDPVNMVLYFLVSAVCGNLLAIVFSLNHNHMPVISKEEAVDMD 367
 QY 331 FSVGQIHEHMTNIRGIIITDFFGGLNYQIEHHLWPTLRPHNLTAVSQVQEQCLCKHNLPI 390
 Db 368 FETKQIITGRDHPGLFANWFTGGLNYQIEHHLFSPMRHNFESKIQAPAVETLCKKNVRY 427
 QY 391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
 Db 428 HTTGMEIGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 2
 W95504
 ID W95504 standard; peptide: 457 AA.
 AC W95504;
 DT 26-MAR-1999 (first entry)
 DE Mortierella alpina delta 6 desaturase.
 KW Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed.
 OS Mortierella alpina.
 PN W09846764-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07421.
 PR 24-OCT-1997; US-956985.
 PR 11-APR-1997; US-833610.
 PR 11-APR-1997; US-834033.
 PR 11-APR-1997; US-834855.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 DR WPI; 99-080739/07.
 DR N-PSDB; X00889.
 PT Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 PS Claim 7; Fig 3A-E; 210pp; English.
 CC This represents a Mortierella alpina delta 6 desaturase. The invention
 CC relates to a nucleic acid construct that contains at least one of the
 CC nucleotide sequences (X00889 to X00891) encoding M. alpina delta 6,
 CC delta 12 and delta 5 desaturases (W95504 to W95506) respectively, coupled
 CC to an expression control sequence functional in plants. Recombinant plant
 CC cells containing at least one DNA encoding a M. alpina fatty acid
 CC desaturase (FAD), can be used for the production of polyunsaturated fatty
 CC acid (PUFA). These recombinant cells or plants containing them are used
 CC to produce oils such as linoleic acid, arachidonic acid, gamma-linolenic
 CC acid, dihomo-gamma-linolenic acid, stearidonic acid and eicosapentaenoic
 CC acid (EPA). These plant oils are used: (i) to treat malnutrition; (ii) in
 CC infant feeding formulas, or dietary supplements or substitutes, for use
 CC in humans or animals; (iii) for treating disorders associated with
 CC inadequate consumption or production of PUFA (or their metabolites such
 CC as prostaglandins), e.g. restenosis after angioplasty, inflammation,
 CC AIDS, rheumatoid arthritis, psoriasis, osteoporosis, cancer, eczema,
 CC diabetes; (iv) as cosmetics, and (v) as animal feeds. Fragments of the

CC DNA are used as probes to isolate related coding sequences. Recombinant
 CC plants can produce high yields of PUFA, since new pathways can be created
 CC and unwanted ones suppressed. Plants can be engineered to express oils of
 CC particular PUFA composition, e.g. one similar to that in human milk, and
 CC product recovery is simpler than with e.g. fish.
 SQ Sequence 457 AA;

Query Match 27.6%; Score 631; DB 1; Length 457;
 Best Local Similarity 33.0%; Pred. No. 9.5e-66;
 Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

QY 2 KSKRQALSPLOLM--EQYDVSNAVNFHFGGABIIENYQGRDATDAPVWVHFOEAFDKLK 59
 Db 23 EGKDAEAPFLMIIDNKVDYDFEVPDPHFGS-VILTHVGKDGTDVDTFHPAAAWETL- 81
 QY 60 RMPKINPSPFLPQAAVNEAQEDF-----RKLEELIATGMEDASPLWYSKISTT 110
 Db 81 -----ANFVV---GDIDESDRDIKNDDFAAEVRKLTFLFQSLGYDSSKAYTAFKVSFN 131
 QY 111 LGLVGLYFLMVOYOM-----YFIGAVLLGMHYOQMGWLSHDICHOTKNNWNNVLGL 165
 Db 132 LCIWGLSTVIVAKWGOTSTLANVLSAALLGLFWOCCGLAHDFLHHQVQDFRFGWDLFGA 191
 QY 166 VFGNGLOGFVTCWKDRHNAHSATNVQGHDPDIDNLPPLAWSDEDDVTRASPI----- 219
 Db 192 FLGGVCGGFSWKKHNTTHAAPNVHGEDPDIDTHTPLTWSEHALEMESDVPDEELTR 251
 QY 219 --SRKLIQOQYVFLVICILLRFTWCFCQVLTVRSLKDRDNQFYRSQYK-----BAIG 270
 Db 252 MWSRFVNLQNTWYFPLSFAUSWCLQSILFVLP-----NGQAHKPSGARVPISLVBQLS 307
 QY 271 LALHWTLKALFLHFFMPSILTSLLVFEVSELVGGFIAIVFMNHYPLEKIGDPVWDGHC 330
 Db 308 LAHWHTWYLTATMFLFKDPVNMVLYFLVSAVCGNLLAIVFSLNHNHMPVISKEEAVDMD 367
 QY 331 FSVGQIHEHMTNIRGIIITDFFGGLNYQIEHHLWPTLRPHNLTAVSQVQEQCLCKHNLPI 390
 Db 368 FETKQIITGRDHPGLFANWFTGGLNYQIEHHLFSPMRHNFESKIQAPAVETLCKKNVRY 427
 QY 391 RNPPLPHEGLVILLRYLAVFARMAEKOPA-----GKA 421
 Db 428 HTTGMEIGTA-----EVFSRLNEVSKAASKMGKA 456

RESULT 3
 W85121
 ID W85121 standard; Protein: 457 AA.
 AC W85121.
 DT 11-FEB-1999 (first entry)
 DE A delta-6 desaturase enzyme amino acid sequence.
 KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846765-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07422.
 PR 11-APR-1997; US-833610.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 DR WPI; 99-009334/01.
 DR New nucleic acid encoding delta5 and other desaturase enzymes -
 PT useful in production of oils of increased arachidonic acid content.
 PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
 PS Disclosure: Pages 95-96; 153pp; English.
 CC The present sequence represents a fatty acid delta-6 desaturase enzyme.
 CC The specification describes methods for desaturating a fatty acid and

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OM protein - protein search, using sw model

Run on: February 25, 2000, 04:45:46 ; Search time 38.64 Seconds
(without alignments)
258.684 Million cell updates/sec

Title: PCT-US99-28655-4
Perfect score: 2283
Sequence: 1 MKSRQALSPQLMEQTYDV.....LRYLAVFARMAEKOPAGKAL 422

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36.*

Word size : 0

Number of hits that pass the threshold : 188963

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	631	27.6	457	1	W84137	A delta-6 desaturase
2	631	27.6	457	1	W95504	Mortierella alpina
3	622	27.2	457	1	W85121	A delta-6 desaturase
4	565	24.7	355	1	W84139	Desaturase enzyme
5	439.5	19.3	448	1	R98455	Borage delta-6-des
6	439.5	19.3	448	1	W67471	Borage delta-6 des
7	439.5	19.3	448	1	W88130	Borage delta-6 des
8	430.5	18.9	446	1	W85122	A delta-6 desaturase
9	421.5	18.5	746	1	W84156	Human desaturase e
10	421.5	18.5	746	1	W85135	A desaturase enzyme
11	421.5	18.5	753	1	W95514	Amino acid sequenc
12	310	13.6	608	1	W84155	Human desaturase e
13	310	13.6	608	1	W85134	A desaturase enzyme
14	310	13.6	615	1	W95513	Amino acid sequenc
15	277.5	12.2	252	1	W84141	Desaturase enzyme
16	249.5	10.9	446	1	W85119	A delta-5 desaturase
17	249.5	10.9	446	1	W95506	Mortierella alpina
18	247	10.8	555	1	W84154	Human desaturase e
19	247	10.8	555	1	W85133	A desaturase enzyme
20	247	10.8	562	1	W95512	Amino acid sequenc
21	244	10.7	306	1	W84153	Human desaturase e
22	244	10.7	306	1	W95132	A desaturase enzyme
23	244	10.7	306	1	W95511	Amino acid sequenc
24	239	10.5	359	1	R34102	Bacterial delta-6-
25	239	10.5	359	1	R98456	Synechocystis delt
26	239	10.5	359	1	W85123	A delta-6 desaturase
27	218	9.5	365	1	W85124	A delta-6 desaturase
28	200	8.8	131	1	W84143	Desaturase enzyme
29	185	8.1	211	1	W84150	Human desaturase e
30	185	8.1	211	1	W85130	A desaturase enzyme
31	185	8.1	218	1	W95509	Amino acid sequenc
32	176	7.7	143	1	W84145	Desaturase enzyme
33	175	7.7	140	1	W84149	Schizochytrium sp.
34	175	7.7	140	1	W85128	A putative partial
35	175	7.7	140	1	W95518	M. alpina desaturase
36	152	6.7	87	1	W84144	Desaturase enzyme
37	148	6.5	382	1	W31740	Delta-12 desaturase
38	147	6.4	312	1	W95095	Synechocystis sp.
39	144.5	6.3	418	1	R60501	Linoleic-acid-desa

Sequence of soybean
Microsomal delta-1
Amino acid sequenc
Phaeodactylum tric
A putative desaturase
Fatty acid desaturase

40 140 6.1 379 1 R53699
41 138.5 6.1 384 1 W24998
42 138.5 6.1 384 1 W94050
43 138 6.0 102 1 W84147
44 138 6.0 102 1 W85126
45 138 6.0 102 1 W95516

ALIGNMENTS

RESULT 1

W84137
ID W84137 standard; Protein; 457 AA.
AC W84137;
DE 15-FEB-1999 (first entry)
KW Fatty acid; delta-6 desaturase;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Mortierella alpina.
PN W09846763-A1.
PD 22-OCT-1998.
PF 10-APR-1998; U07126.
PR 11-APR-1997; US-834655.
PA (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P,
PI Thurmond J;
DR WPI; 98-594582/50.
DR N-PSDB; V63624.
PT New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
PS Claim 3; Fig 3A-E; 165pp; English.
CC The present sequence represents a Mortierella alpina fatty acid delta-6
CC desaturase enzyme. The enzyme sequence is used in the methods of
CC the invention. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. The present desaturase is an enzyme
CC which introduces a double bond carbons 6 and 7 from the carboxyl end of
CC a fatty acid molecule. The enzyme can be used for desaturating fatty
CC acids. The enzyme can be used to produce polyunsaturated fatty acids,
CC which can be used for treating malnutrition, in pharmaceutical
CC compositions, in cosmetics or in animal feed. The polyunsaturated fatty
CC acids can be used for treating e.g. restenosis after angioplasty,
CC inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes
CC or eczema or reduce blood pressure. They can also be used to inhibit
CC platelet aggregation, cause vasodilation, lower cholesterol levels,
CC inhibit proliferation of vessel wall smooth muscle and fibrous tissue,
CC reduce or prevent gastro-intestinal bleeding and other side effects
CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
CC and chronic fatigue after viral infections, treat AIDS, multiple
CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
CC disorders.
SQ Sequence 457 AA;

Query Match 27.6%; Score 631; DB 1; Length 457;

Best Local Similarity 33.0%; Pred. No. 9.5e-66;

Matches 150; Conservative 76; Mismatches 173; Indels 56; Gaps 11;

OY 2 KSKRQALSPQLM--EQTVDYSAWVNFHPGGAEIENYOGKRDATDFWVWHQAEADKLK 59

DB 23 EGKDKAEAFPLMIIDKNVYDFREFVDPDPGGG-VILTHVKGDTGVDFTDFHPEAAWETL 81

OY 60 RMPKINPSELPQQAQVNAEQEDF-----RKLRELIATGMFDASPLWYSYKIST 110

DB 81 -----ANFYV---GDIDESRDINDPFAAEVRKLTFLQSLGYDSSKAYAFKVSFN 131

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OY 392 TMRHNTVMPVKFEAAANGLPY 416
    ||||| : ||| : |||
Db 390 TMRHNLKHIAPLVKSLCAKHGIEY 414

RESULT 15
Q920R9 PRELIMINARY; PRT; 444 AA.
AC Q920R9
DT 01-MAY-1999 (TMRHNTVMPVKFEAAANGLPY 416, Created)
DT 01-MAY-1999 (TMRHNTVMPVKFEAAANGLPY 416, Last sequence update)
DT 01-NOV-1999 (TMRHNTVMPVKFEAAANGLPY 416, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99085046.
RA CHO H.P., NAKAMURA M.T., CLARKE S.D.;
RT "Cloning, expression, and nutritional regulation of the mammalian
RL Delta-6 desaturase.";
DR EMBL; AF126798; AAD20017.1; -.
DR HSP; P00171; 3B5C.
SQ SEQUENCE 444 AA; 52387 MW; F6F9668B CRC32;

Query Match 15.3%; Score 373; DB 11; Length 444;
Best Local Similarity 25.8%; Pred. No. 4.9e-24;
Matches 124; Conservative 68; Mismatches 179; Indels 110; Gaps 17;

OY 4 REQHEPFIKIDKWCODDAVL-----RSHPGG-SAITTYKNMDATTVFHTFGSK 56
Db 22 RWEIQKHNLT-RWLVIDRKVNVTKWSQRHPGGHVRVGHYSGEDATDAFRAHLDLD 80
OY 57 EAYQWLTELK-KECPTQPEIPDKDDPIKIGIDVNMGTNFNISEKRSQAINKSFIDLRMR 115
Db 81 FVGFELPGLLIGELAPEP-----SIDRCKSSQITDFALAKT 119
OY 116 VRAEGLMDGSLFYRKILETIFILFAFL--QYHTYLP---SAILMGVAMQOLGWL 170
Db 120 AEDNLFKTNHLLFFLLSHIIVMESLAWFILSYFGTGWITLVTAFLVATSAQAGWLQ 179
OY 171 HEFAHOLFKNRYNDLASYVGNFLOGFSGGKKEOHNVHHAATNVVGRDGLDLVPFY 230
Db 180 HDYGLSVYKSIWNHVVHKEVIGHLKGSANWNNRHFQHHAKPNIFHKDPDI----- 234
OY 231 ATVAEHLNNSQDSWVMTLFRWQ-----HVHWTFML---PFLRLSWLIQS 272
Db 234 -----KSLHVFVLGEMQPLEYGGKKLVLPYNNHQHEFFLIGPPLL----- 275
OY 273 IIFVSQMPHYDYIRNTAIYEQVGLSHWAMSLGQLYFLPDNSTRIMFF-LVSHLVG-- 330
Db 275 -----IPMYFQYQIIMTISRDRWDVLAWAIS---YIMRFFTYIPFYGILGALVFN 324.
OY 330 --GFLLSH---VTFNHYSVEKALSNSNMSNYACLOIMTRNMRPGRFIDNLWGGLNY 383
Db 325 FIRELESNFWVWQMHNLVNE---IDLHYRDMFSSQAAATCNVEOSFFNDFSGHLNF 381
OY 384 QIEHHLFPTMRHNTVMPVKFEAAANGLPYVVDYFTGFWELEIOFRNIANVAKL 443
Db 382 QIEHHLFPTMRHNLKHIAPLVKSLCAKHGIEY-----EKPLLRALIDIVSSLK 431
OY 444 K 444
Db 432 K 432

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Qy 129 ----YIRKILETIFILFAFYLO-----YHTYILPSAILMGVAAQOGLWLTHEFAH 175
Db 127 ERVGHTRKFLVAMSVLFIALCYVLACSSGTAHMF---AGGLGFIWISQGWIGHDSGH 183
Qy 176 HOLFKRNYNDLASVYFNGFLQSGSGGWKQKHNVHHAATNVVGRDGLDLVPFYATVAE 235
Db 184 HOITRHPALNLLQVYVSGNCLTGLGIAMWKNHNTHHISCSNLDHDPDLQHLPLFAVSTK 243
Qy 236 HLNVSQDSWMTL-----FRQHVHMTF--MLPEURLSLWLSQIIF-VSQMTHYXD 285
Db 244 LFNLMNSVCYERTLAFDAISAEFFVSQHWTFYPVNGFARINLLVOSIVFLITQKV---- 300
Qy 286 YRNTAIYEQVGLSLHWASLGOLYFLPDWSTRIMEFLVSHLVGGFLLSHV-VTPNHYSV 344
Db 300 ---RQRWEIAGVAAFWYVYVLLVSLCLPNWVERVAFVLAFFVITG--IQHVQFCLNHFSS 354
Qy 345 EKFSALSSNIMNYACLOIMTTRNMRPGRFIDWLAGGLVNOYIEHHLFTPMRHNLTVMPL 404
Db 355 AVY-VGPPKGNDFEROTAGTLDIKCSPMDMDFHGGLOFQVEHHLFPRLPRCHRYRWAPI 413
Qy 405 VKEFAAANGLPY 416
Db 414 VRDLCKKHGLSY 425

RESULT 13
Q92RP8 ID Q92RP8 PRELIMINARY; PRT; 449 AA.
AC Q92RP8 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TremBLrel. 12, Last annotation update)
DE DELTA-8 SPHINGOLIPID DESATURASE.
GN SLD1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euryhalophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Brassica.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DRAKKAR; TISSUE=RIPENING EMBRYOS;
RX MEDLINE; 99003197.
RA SPERLING P., ZAEHRINGER U., HEINZ E.;
RT "A sphingolipid desaturase from higher plants. Identification of a new
RT cytochrome b5 fusion protein.";
RL J. Biol. Chem. 273:28590-28596(1998).
DR EMBL; AJ224160; CAA11857.1; -.
DR HSSP; P00173; 1AQA.
DR MENDEL; 34704; Brana;2419;34704.
SQ SEQUENCE 449 AA; 51490 MW; F9BB69EE CRC32;
```

```
Query Match 15.5%; Score 378.5; DB 10; Length 449;
Best Local Similarity 24.9%; Pred. No. 1.7e-24;
Matches 109; Conservative 84; Mismatches 173; Indels 71; Gaps 17;

Qy 5 BOEHEP--FFKIDGKWCQIDDAVLRSHPG-SAITTKNMDDATTVEHFTHTGSKAEYOW 61
Db 16 KKHNPQGLWISIQGVYDVSHV-KSHPGGEAAILNLAGQDVDAFIAPHGT----AW 70
Qy 62 LTELKKECTOPEIPIDKIDGIDVNMGTFTNISEKRSQKSFDTLDRMRVRAEGL 121
Db 71 -----RHELENLHG-YHVKHVSDVSRDYLAAEFKRGRL 106
Qy 122 MDGSPFLYIRKILETIFTI-LFAFYLYQHTY-----YLPsAILMGVAAQOGLWLI 170
Db 107 FD-----KKGHVTLITLCVAAMLAAYVGVVACTSIWAHLISAVLLGLLWISAYVG 159
Qy 171 HEFAHOLFKNRYNDLASVYFNGFLQSGSGGWKQKHNVHHAATNVVGRDGLDLVPY 230
Db 160 HDSGHYNTSTKPCNKVQLLSGNCITGISIAWKNWTHNAHHSNLSLDHDPDLQHIPVL 219
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Qy 231 ATVAEHLNNYSQDSWMTL-----FRQHVHMTFMLPFL---RLSWLQSIIFVSOMP 280
Db 220 AVSNKFFKMTSREYGRKLTDPDLAREFLISYQHMSF-YPIMCVGRINFLIOTLLLSFR- 278
Qy 281 THYDYIYRNTAIYEQVGLSLHWASLGOLYFLPDWSTRIMEFLVSHLVGGFLLSHV-VTF 339
Db 278 RYVDPDRALNIA-----GILVFWTWFPPLVSLFPMOERLIIFVLSMAYTA--IQHVQCL 330
Qy 340 NHYSVEKFPALSSNIMNYACLOIMTTRNMRPGRFIDWLAGGLVNOYIEHHLFTPMRHNLN 399
Db 331 NHFAADVYTGPPN-GNDWFKEQTAGTLDISCRSYMDWFFGGLOFQLEHHLFPRLPRCHLR 389
Qy 400 TVMPLVKEFAAANGLPY 416
Db 390 GVSPLYVQELCKKHNLPLY 406

RESULT 14
O95864 ID O95864 PRELIMINARY; PRT; 444 AA.
AC O95864 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TremBLrel. 12, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99085046.
RA CHO H.P., NAKAMURA M.T., CLARKE S.D.;
RT "Cloning, expression, and nutritional regulation of the mammalian
RT Delta-6 desaturase.";
RL J. Biol. Chem. 274:471-477(1999).
DR EMBL; AF126799; AAD20018.1; -.
DR HSSP; P00171; INDB.
SQ SEQUENCE 444 AA; 52259 MW; 78230925 CRC32;
```

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Query Match 15.4%; Score 374.5; DB 4; Length 444;
Best Local Similarity 26.5%; Pred. No. 3.7e-24;
Matches 118; Conservative 70; Mismatches 166; Indels 91; Gaps 17;

Qy 6 QEHEPFFIKIDGKWCQIDDAVLRL-----SHPGGS-AITTKNMDDATTVEHFTHTGSKEA 58
Db 27 QKHN---LRTD-RWLVIDRKVYNITKWSIQHPGGQGVIGHYAGEDATDAFRAHPDLEFV 82
Qy 59 YOWLT-----ELKKECTOPEIPIDKIDDPKIGIDVNMGTFTNISEKRSQKINQSFDTLR 113
Db 83 GKFLAPLLIGELAPEPSQD-----HGKNSKITEDFRALR 117
Qy 114 MVRAGEHMDGSPFLYIRKI-----LETI--FTILFAFYLYQHTYLP---SAILMGVAAW 163
Db 118 KTAEDMNLKFNHNVFFLLLLAHIALESIAMTV---FY--FGNWIPPLITAFVLATSQ 172
Qy 164 QOLGLWLIHEFAHOLFKNRYNDLASVYFNGFLQSGSGGWKQKHNVHHAATNVVGRDGD 223
Db 173 AQAGWLQHDYGHLSVYRKPKWNHLVKFVIGHLKASANWNNHRRFQHHAKNFIHKDPD 232
Qy 224 LDLVPFYATVAEHLNNYSQDSWMTLFRQHVHMTFMLPFLRLSWLQSIIFVSOMPTHY 283
Db 233 VNMLHVFVGEWQPEYGGKLLKYLPNHQHVEYFFLPGPLLPYFOYIIM----- 286
Qy 284 YDYIYRNTAIYEQVGLSLHWASLGOLYFLPDWSTRIMEFLVSHLVGG-----FLLSH 335
Db 286 -----THVHKNVWDLAWAVS---YIRFEITYIPFY---GILGALLFLNFIREFLSH 332
Qy 336 ---YVTNHHYSVEKFSALSSNIMNYACLOIMTTRNMRPGRFIDWLAGGLVNOYIEHHLFP 391
Db 333 WFWVWYQNHVME---IDQEAIRDWFFSSQLTATCNVEQSFENDFSGHLNFQIEHHLFP 389
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QY 181 NRYNDLASIFVGNFLOGSSGGKQHNHHAATNVVGRDGLDLPFYATVAEHLNLY 240
DB 181 NRYNDLASIFVGNFLOGSSGGKQHNHHAATNVVGRDGLDLPFYATVAEHLNLY 240
QY 241 SÖDSWMTLFRWQHVHTFMLPFLRLSWLLOSIIFVSQMPHYDYRYNTAIYEQVGLSL 300
DB 241 SÖDSWMTLFRWQHVHTFMLPFLRLSWLLOSIIFVSQMPHYDYRYNTAIYEQVGLSL 300
QY 301 HWAWSLQGLFLPDWSTRIMFFLVSHLVGGFLLSHVTFNHSYVEKFSALSNINACL 360
DB 301 HWAWSLQGLFLPDWSTRIMFFLVSHLVGGFLLSHVTFNHSYVEKFSALSNINACL 360
QY 361 QIMTRNMRGPRFIDWLWGLGNYOIEHHLFPTMPRHNLNTVMPVKFAAANGLPYVDD 420
DB 361 QIMTRNMRGPRFIDWLWGLGNYOIEHHLFPTMPRHNLNTVMPVKFAAANGLPYVDD 420
QY 421 YFTGFWEIEIOFRNIANVAALKTKKIA 447
DB 421 YFTGFWEIEIOFRNIANVAALKTKKIA 447

RESULT 2
Q94044 PRELIMINARY; PRT; 454 AA.
AC Q94044;
DT 01-FEB-1997 (T-EMBLrel. 02, Created)
DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)
DE 01-JAN-1999 (T-EMBLrel. 09, Last annotation update)
DE T13F2.1 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX SWINBURNE J.;
RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FULTON L.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., JEROME L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMAILDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL; 281122; CAB03352.1;
SQ SEQUENCE 454 AA; 53160 MW; D7FD13FA CRC32;

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Query Match 99.4%; Score 2421.5; DB 5; Length 454;
Best Local Similarity 98.5%; Pred. No. 4.2e-199;
Matches 447; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

QY 1 MYLREQEHPFIKIDGKWCQDDAVLRSHPGSAITTYKNMDATTVFHTFTGSKYAYO 60
DB 1 MYLREQEHPFIKIDGKWCQDDAVLRSHPGSAITTYKNMDATTVFHTFTGSKYAYO 60
QY 61 WLTELKKECTOPEIPDKDDPIKIDVNMGTFTNISEKRSQAINKSTDLRMVRAEG 120
DB 61 WLTELKKECTOPEIPDKDDPIKIDVNMGTFTNISEKRSQAINKSTDLRMVRAEG 120
QY 121 LMDGSPFYIRKILETIFTLFAFYLYHTYLLPSAILMGVAQQLGWLHIEFAHHQLFK 180
DB 121 LMDGSPFYIRKILETIFTLFAFYLYHTYLLPSAILMGVAQQLGWLHIEFAHHQLFK 180

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QY 181 NRYNDLASIFVGNFLOGSSGGKQHNHHAATNVVGRDGLDLPFYATV 233
DB 181 NRYNDLASIFVGNFLOGSSGGKQHNHHAATNVVGRDGLDLPFYATV 240
QY 234 AEHLNNYSQDSWMTLFRWQHVHTFMLPFLRLSWLLOSIIFVSQMPHYDYRYNTAIY 293
DB 241 AEHLNNYSQDSWMTLFRWQHVHTFMLPFLRLSWLLOSIIFVSQMPHYDYRYNTAIY 300
QY 294 EQVGLSLHWAWSLQGLFLPDWSTRIMFFLVSHLVGGFLLSHVTFNHSYVEKFSALSN 353
DB 301 EQVGLSLHWAWSLQGLFLPDWSTRIMFFLVSHLVGGFLLSHVTFNHSYVEKFSALSN 360
QY 354 MSNTACLOIMTRNMRGPRFIDWLWGLGNYOIEHHLFPTMPRHNLNTVMPVKFAAANG 413
DB 361 MSNTACLOIMTRNMRGPRFIDWLWGLGNYOIEHHLFPTMPRHNLNTVMPVKFAAANG 420
QY 414 LPYVDDYFTGFWEIEIOFRNIANVAALKTKKIA 447
DB 421 LPYVDDYFTGFWEIEIOFRNIANVAALKTKKIA 454

RESULT 3
O61388 PRELIMINARY; PRT; 443 AA.
AC O61388;
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
DE 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
DE DELTA6-FATTY-ACID-DESATURASE.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97268723.
RA SAYANOVA O., SMITH M.A., LAPINSKAS P., STOBART A.K., DOBSON G.,
RA CHRISTIE W.W., SHEWRY P.R., NAPIER J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98149727.
RA NAPIER J.A., HEY S.J., LACEY D.J., SHEWRY P.R.;
RT "Identification of a Caenorhabditis elegans Delta6-fatty-acid-
RT desaturase by heterologous expression in Saccharomyces cerevisiae.";
RL Biochem. J. 330:0-0(0).
DR EMBL; AF031477; AAC15586.1;
SQ SEQUENCE 443 AA; 51740 MW; EE44468D CRC32;

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Query Match 44.9%; Score 1092.5; DB 5; Length 443;
Best Local Similarity 46.3%; Pred. No. 1.6e-85;
Matches 201; Conservative 84; Mismatches 140; Indels 9; Gaps 4;

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QY 13 IKIDGKWCQDDAVLRSHPGSAITTYKNMDATTVFHTFTGSKYAYOVLTELKKECTPQ 72
DB 12 MKVDGKNLYSELVYKHPGAGVIOYRNSDATHIFAFHEGSSQAQKOLDLKKHGEHD 71
QY 73 EPEIPDKDDPIKID--DVNMGTFTNISEKRSQAINKSTDLRMVRAEGMDGSPFYI 130
DB 72 E----FLEKQLEKRLDKVDINVSAYDSVAQEKKNVSEKLEKRLQKLDHDLGKANEYFL 127
QY 131 RLITFTILFAFYLYHTYLLPSAILMGVAQQLGWLHIEFAHHQLFKRYNYDLASY 190
DB 128 FRAISTLSIMAFAYLYQYLGWITSACILALAWQFGWLTHFCHQOQTKRPNLNTISL 187
QY 191 FYGNFLQFGSSGGKQHNHHAATNVVGRDGLDLPFYATVAEHLNLY--SÖDSWMT 248
DB 188 FFGNFLQFGSSGGKQHNHHAATNVVGRDGLDLPFYATVAEHLNLY--SÖDSWMT 248

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GenCore version 4.5
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OM protein - protein search, using sw model

Run On: February 24, 2000, 22:03:17 ; Search time 51.75 Seconds
(without alignments)
598.886 Million cell updates/sec

Title: PCT-US99-28655-2
Perfect score: 2435
Sequence: 1 MVLREQHEPFFIKIDGKWC.....ETQPRNIANVAAKLTKKIA 447

Scoring table: BLOSUM62

Searched: 225878 seqs, 69334122 residues

Database : SPTREMBL_12:*

Word size : 0

Number of hits that pass the threshold : 225878

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	2435	100.0	447	5	Q9XTB7	Q9xtb7 caenorhabdi
2	2421.5	99.4	454	5	Q94044	Q94044 caenorhabdi
3	1092.5	44.9	443	5	O61388	O61388 caenorhabdi
4	1073.5	44.1	473	5	Q23221	Q23221 caenorhabdi
5	578.5	23.8	525	10	Q92NW2	Q92nw2 physcomitre
6	422.5	17.4	449	10	O82348	O82348 arabidopsis
7	412.5	16.9	448	10	O04353	O04353 borago offi
8	402.5	16.5	458	10	Q43469	Q43469 hellanthus
9	402	16.5	449	10	Q92RP7	Q92rp7 arabidopsis
10	401.5	16.5	444	4	O60427	O60427 homo sapien
11	397	16.3	446	10	Q92TY9	Q92ty9 ricinus com
12	390.5	16.0	469	10	Q92T08	Q92t08 triticum ae
13	378.5	15.5	449	10	Q92RP8	Q92rp8 brassica na
14	374.5	15.4	444	4	O95864	O95864 homo sapien
15	373	15.3	444	11	Q920R9	Q920r9 mus musculu
16	372.5	15.3	445	4	O9X500	O9x5q0 homo sapien
17	367	15.1	444	11	Q92122	Q92122 rattus norv
18	364.5	15.0	446	10	Q92T29	Q92tz9 arabidopsis
19	316.5	13.0	311	4	Q9Y3X4	Q9y3x4 homo sapien
20	266.5	10.9	345	2	Q9X8W4	Q9x8w4 streptomyce
21	241	9.9	467	5	O96099	O96099 dictyosteli
22	231	9.5	446	3	O74212	O74212 mortierella
23	216.5	8.9	464	5	O9Y1W0	O9y1w0 dictyosteli
24	211	8.7	368	2	O54795	O54795 spirulina p
25	173	7.1	352	4	O60426	O60426 homo sapien

26	152.5	6.3	332	10	Q9ZPH4	Q9zph4 arabidopsis
27	150	6.2	379	10	O22628	O22628 arachis hyp
28	149.5	6.1	287	8	O19891	O19891 cyanidium c
29	144.5	5.9	352	2	O34653	O34653 bacillus su
30	142	5.8	385	10	O23955	O23955 gossypium h
31	141.5	5.8	312	10	Q92NW8	Q92nw8 brassica ra
32	140.5	5.8	427	2	O05874	O05874 mycobacteri
33	140.5	5.8	379	10	O65772	O65772 crepis pala
34	140	5.7	361	2	O85776	O85776 rhizobium l
35	139.5	5.7	347	2	O55231	O55231 synechococc
36	138	5.7	387	10	O41131	O41131 ricinus com
37	137	5.6	383	10	O41305	O41305 solanum com
38	137	5.6	383	10	O23956	O23956 gossypium h
39	136.5	5.6	359	2	O55240	O55240 synechocyst
40	133	5.5	362	3	O59715	O59715 schizosacch
41	132.5	5.4	384	10	O81094	O81094 lequerella
42	132	5.4	323	4	O15121	O15121 homo sapien
43	131.5	5.4	378	10	O24499	O24499 hellanthus
44	131.5	5.4	384	10	O92PI2	O92pi2 brassica ca
45	131	5.4	350	2	O44503	O44503 anabaena va

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	447 AA.
Q9XTB7	AC	Q9XTB7;		
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)		
DE	DELTA5-FATTY ACID DESATURASE.			
GN	FAT-4 OR DES-5.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;			
OC	Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 99059458.			
RA	WATTS J.L., BROWSE J.:			
RT	"Functional identification of a fatty acid delta5 desaturase gene from			
RT	Caenorhabditis elegans."			
RL	Arch. Biochem. Biophys. 362:175-182(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=C.elegans;			
RX	MEDLINE: 99059458.			
RA	STOBART A.K.:			
RT	"Functional identification of a fatty acid delta5 desaturase gene from			
RT	Caenorhabditis elegans."			
FEBS	Let. 439:215-218(1998).			
DR	EMBL: AF114440; RAD13294.1;			
DR	EMBL: AF078796; AAC93143.1;			
SQ	SEQUENCE 447 AA; 52348 MW; E62A9A02 CRC32;			

Query Match 100.0%; Score 2435; DB 5; Length 447;
Best Local Similarity 100.0%; Pred. NO. 2.9e-200;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVLREQHEPFFIKIDGKWCQIDAVLRSHPGGSAITTYKNMDATTVFHTFTGSKYAY 60	
Db	1	MVLREQHEPFFIKIDGKWCQIDAVLRSHPGGSAITTYKNMDATTVFHTFTGSKYAY 60	
QY	61	WLTELKKECTQBPETDPIKDDPIKIGIDDYVMGTFTNSEKRSQINKSFDTLNRVRAEG 120	
Db	61	WLTELKKECTQBPETDPIKDDYVMGTFTNSEKRSQINKSFDTLNRVRAEG 120	
QY	121	LMDSPLFYRKILETFTILFAFYLOHYHYLPSATLMGVAMQOLGWLHFEFAHQLFK 180	
Db	121	LMDSPLFYRKILETFTILFAFYLOHYHYLPSATLMGVAMQOLGWLHFEFAHQLFK 180	

Fri Feb 25 11:19:47 2000

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Db 201 RPYDRFACHYDPYPIYNNR-ERLQIFISDAGVLGVCYLL-----YRIALVKGLAWL 251
Qy 328 -----VGGFL-----LSHV-VTFNHYSVEKFALSSNIMSNYACLOIMTTRNMRPG 371
Db 252 VCVYGVPLLVVNGFLVLTITYLQHTHPSLPHYDSTEW----- 288
Qy 372 RFIDWLWGGL-----NYQIEHHLEFTMPRHN-----LNTVMPLVKFEFA 409
Db 288 ---DWLREGALATCDRDYGVNLKVFHNITDTHVYVHHLESTWPHYNAMEATKAVKELLGDYY 344
Qy 410 AANGLPYMVDYFTGFWEIEQ 431
Db 345 QFDGTP-----IYKEMWREAKE 361
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Search completed: February 24, 2000, 22:01:38
Job time: 17315 sec

A:Reference number: 216895
A:Accession: T09880
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-385 <LIU>
A:Cross-references: EMBL:X97016; NID:e991751; PID:e242368
A:Experimental source: cultivar Deltapine-16
C:Function:
A:Description: Introduces a cis double bond at omega-6 position of oleic acids
C:Superfamily: omega-3 fatty acid desaturase

Query Match 5.8%; Score 142; DB 2; Length 385;
Best Local Similarity 19.2%; Pred. No. 0.0003;
Matches 85; Conservative 56; Mismatches 119; Indels 182; Gaps 22;
QY 83 PIKIDVNMGT-----FNISEKRS-----QINKST-----DLRVRVREG 120
DB 8 PIDGIKENGRSVNRPPIKPPFTLGQIKQAIHPHCFFRRSLRFSYVVDLCL----- 62
QY 121 LMDGSPFYIRKILETITILFAF-----YLOVHTY-LPSAILMGVAVQOLGWL-HE 172
DB 62 ----ASFYY-----TATSFHFLPQPFYSIANPVVWLOGCILTGV-----WVIAHE 105
QY 173 FAHOLFKNRYND-----LASYFVGNFLQSGGKQHOHNHHAATNVVGRDG 222
DB 106 WGHHAERDYQVDDTVGLILHSALLVPYF-----SWKISHRRHSNTGSMERDE 154
QY 223 DLDLVP--FYATVAEHLNNYSQDSWVWTLFRQVHWHVTFMPLFRLSLWLLQSIIFVSOMP 280
DB 155 VFVPKPSKLSCFARYLNN--PPGRVSLVTLTLGWPMYLAFA-----NVS 198
QY 281 THYD-----YVRNTAIVBOVGLSLHWAWSLQGLYFLPDWSTRI 319
DB 199 GRYDRLASHNPNPGPIYSDRLOVYISDGFIVAVIVLYKIAATKGLWLLCYGVPL 258
QY 320 MFFLVSHLVGGFLSHVTVF-----NHYSVEKFASSNIMSNYACLIQMTTRMRPG 371
DB 259 L-----IVNAFLV--LITYLQHTSALPHYDSSEW----- 287
QY 372 RFIDWLWGLL-----NYQIEHLFTMPHNN-----LNTVMPVLKFEA 409
DB 287 ---DWLRCALSTMDRDFGLNKNVFNHTDTHVAHHLFTSTMPHYHAMEATKAIPILGYY 343
QY 410 AANGLPYVMDYFTGFWEIEQ 431
DB 344 PFDGTP-----IYKAWREAKE 360

RESULT 11
G70590
Probable desA3 protein - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C:Accession: G70590
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: G70590
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-427 <COL>
A:Cross-references: GB:A1123456; NID:g3261742; PID:e314467; PID:g2072696
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: desA3

Query Match 5.8%; Score 140.5; DB 2; Length 427;

Best Local Similarity 20.9%; Pred. No. 0.00046;
Matches 52; Conservative 46; Mismatches 134; Indels 17; Gaps 6;
QY 200 SSGGWKEQHN--VHHAATNVVGRDGLDLVPFYATVAEHLNNYSQDSWVWTLFRQVHWH 258
DB 117 SSKHWRYTHNPFVHHKYNILGMDDDVGVMRLVRDQWRKRYNIFNVVNTILAIGFEWG 176
QY 259 FMLPFLRLSLWLLQSIIFVSQMPHTHYDYRYNT---AIYEQVGLSLHWAWSLQGLYFLPDW 315
DB 177 VALQHLKIGKIFKGRADRAAKTRLEFSKAGROVFKDYVAFPAITSLSPGATY----- 232
QY 316 STRIMFVLVSHLVGGFLSHVVTENHY--SVEKEFALSSNI---MSNYACLIQMTTRMRP 370
DB 232 RSTITANVANVINRVNSNAVFCGHPDGAETKTKDIMEKPGKOWTLRQMLGSANENA 291
QY 371 GRFDWLWGGUNYQIEHLEFTMPRHNLNTYMLVPLKEFAAANGLPYVDDYFTGFWEIE 430
DB 292 GPALRFMSGNLCHOIEHLYPDLPSNRLHEISVRREVCDYDLPTTGTGSLVQYVG---K 348
QY 431 QFRNIANVA 439
DB 349 TWRTIAKLS 357

RESULT 12
S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - Synecococcus sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) (mis)
C:Species: Synecococcus sp.
A:Variety: PCC 7002
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanob
A:Reference number: S43770; MUID:94207189
A:Accession: S43771
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:DL3779; NID:g488510; PIDN:BAA02922.1; PID:d1003428; PID:g48
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: Oxidoreductase

Query Match 5.7%; Score 139.5; DB 2; Length 347;
Best Local Similarity 21.0%; Pred. No. 0.00043;
Matches 74; Conservative 54; Mismatches 151; Indels 73; Gaps 14;
QY 110 TDLRMVRAEGLMDGSPFYIRKILETI-----FTIL 141
DB 2 TSVTVRPSATTLLEKHPNLRDLRLDILTLPRSVEINPLKWSRVLLSVAAVVGCYALLAI 61
QY 142: FAFYLOIHTYIYLPSSAILMGVAVQOLGWL-HEFAHQHQLFKNRYNDLASFYVGNFL---Q 197
DB 62 APWYLLLPVWELTGTTLTGTF-----FVIGHDCGRSFRKNNVNLVGHLA--FLPLYI 113
QY 198 FSSGCGKEQHNHHAATNVVGRDGLDLVPFYATVAEHLNNYSQDSWVWTLFRQVHWH 257
DB 114 PFHS--WILHNHHRYIN--NMEDNAWAFTPELYD-----DSPAFIKAVYR----- 159
QY 258 FTMLPFLRLSLWLLQSIIFVSQMPHTHYDYRYNTAIYEQVGLSLHWAWSLQGL-----YF 311
DB 159 ----AIRKGLMWLASVI--HQLKLFENWFAFEGKQOVRFSALEFVITAGIAFAFPMFT 212
QY 312 LPDWSTRIMFVLVSHLVGGFLSHVVTENHYSVEKFASSNIMSNYACLIQMTTRMRPG 371
DB 213 LGVWGV--VKFWLMPVLGWHFMS--TFTLVHHTVPEIPFSYRDKWNEAIAQLSGTVCDDYP 270
QY 372 RFIDWLWGLNVOIEHHLFPPTMPRHNLNTVMPLEFAAANGLPYVDDYFT 423
DB 271 KWVEVLCHDINVHPHHLSTGIPSYNLRKAYASIKQ----NWGEIYETKFS 318

Db 154 --WIWARTLLICLLFIA-FETNILEYVFKWFCPALVVGFG--LCFIDLPHPPFKYTOR 209
 QY 353 IMSNVACIQIMTRNMRGRFIDMLWGLNYQIEHHLPTMP 394
 Db 210 --WHNSCVY-----PSKFLNLAIFQNYHLVHLLWPSAP 241

RESULT 9
 B69901
 fatty-acid desaturase homolog yocE - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998
 C:Accession: B69901
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.;
 C.; Bron, S.; Broutillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.;
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrat
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.;
 Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hull
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lar
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Por
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Sa
 A:Authors: Schleich, S.; Schroter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.
 teuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; U
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoc
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus sub
 A:Reference number: A69580; MUID:98044033
 A:Accession: B69901
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-352 <KUN>
 A:Cross-references: GB:299114; GB:AL009126; NID:g2634230; PID:el185390; PID:g2634
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yocE

Query Match 5.9%; Score 144.5; DB 2; Length 352;
 Best Local Similarity 21.8%; Pred. No. 0.00017;
 Matches 64; Conservative 52; Mismatches 115; Indels 63; Gaps 15;

QY 132 KILET---IFFILFAFYQYHTYLPYSAILMGVAMQQLGWL-----IHEFAHQQLFKNR 182
 Db 31 QLLNTFFPFGWFLAYLSDVSYLLTALTVIA---AGFLTRIFIFHDCCHQSFQK 87
 QY 183 YYNDLASYVGNFLQFGSSGKMKOHNVHAATNVVGRDGLDLPFYFATVAEHLNYSQ 242
 Db 88 RYNHILGLTG-VLTLPFLYQWQSHSIHTHATSSNLDKRGTDI--WMLTVNEYKAASRR 144
 QY 243 DSWVWTLFRQHVHTFMLPFLRLSWLQSI-IFV-----SQMPTHYDYRYNTAI 292
 Db 145 TKLAYRLYR-----NPF--IMFILGYIVFLITRNFKKGARKKRVNTYLTNLA 193
 QY 293 YEQVGLSLHAWMSLQGLYFLPDWSTRIM----FFLVSHLVGG--FLLSHVVFNNHYSVEK 346
 Db 194 ---VALAAACCLIFG-----WQSFLLVQGPFIUSSIQVWMLFYVQHTFEDSFEEAD 243
 QY 347 FALSSNIMSNYACIQ--IMTTRNRPGRFIDMLWGLNYQIEHHLPTMPRHNL 398
 Db 244 -----NWSYVQAAVEGGSFYKLPKLLQLWLTGNYCHVHHLSPKVPNYKL 288

RESULT 10
 T09880
 omega-6 desaturase - upland cotton
 C:Species: Gossypium hirsutum (upland cotton)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
 C:Accession: T09880
 R:Liu, Q.
 submitted to the EMBL Data Library, March 1996

QY 249 LERWQHWTMLPFLRLSLLQSIIFVSQMPHYDYRNTAIYEQVGLSLHWASLQ 308
Db 125 PYHQHXYFFLPGPLLPYFQOILM-----TMIHVKNVDLAWAVS--- 169
QY 309 LYFLPDKWSTTRIMFLVSHLVGG-----FLLSH-----VVFNFHYVEKFASSNMSN 356
Db 169 -YYIRFFITIPFY--GILGALLFLNFIREFLESHEFWVWTQMNHYNE-----IDQEAIRD 221
QY 357 YACLOIMTNNMRPGRFIDMLWGLNGLOIEHLEFPTPRHNLNTVMPVKFAAANGLPY 416
Db 222 WFSQLPATCNQEQSFNDWFSGLHNFQIEHLEFPTPRHNLNHIAPLVKSLCAKHGIEY 281

RESULT 5
S35157
Delta(6)-desaturase - Synechocystis sp.
C:Species: Synechocystis sp.
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
C:Accession: S35157; S76243
R:Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.
Plant Mol. Biol. 22, 293-300, 1993
A:Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synechocystis sp.
A:Reference number: S35157; MUID:93283633
A:Accession: S35157
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <RED>
A:Cross-references: GB:L11421; NID:9349562; PIDN:AAA27286.1; PID:g349563
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, N. K. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
A:Reference number: S74322; MUID:97061201
A:Accession: S76243
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <KAN>
A:Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PID:d1019235; PID:g1653589
A:Experimental source: PCC 6803
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 8.7% Score 211; DB 2; Length 359;
Best Local Similarity 23.4%; Pred. No. 6.1e-10;
Matches 84; Conservative 62; Mismatches 147; Indels 66; Gaps 18;
QY 112 LRMVRA-----EGLMD-GSPLFYIRKILETIFITILFAFYLOYHTYYP-----SAIL 158
Db 19 LNRVDAYFAEHLGTQRDNPSMY-----LKTLLIWLFSAWAFVLFAPVFPVRLGCMV 74
QY 159 MGVAQOQLGWLIIHEFAHQLFKNRYNDLASVFNGLQSSGGWKEQHN-VHHAATNV 217
Db 75 LAIALAFAFNVGHADANAYSSNPINRVLGMTYDFV-GUSSFLWRVHRNVLHTYINI 133
QY 218 VGRGDL--DLVPFVATVAEHLNNYSQDSWVNTLFRQHWV-WTFLPFLRLSLLQSI 274
Db 134 LGHDEVEHGDGAVRNSPQEHVG-----IVRFQOYINGLYL-FIPFYWFLYDY 182
QY 275 FVSQMPHYDY-----YRNTAIYEQVGLSLHWASLQGLYFLPDWSTTRIMFLVSHLVGG 330
Db 183 LVLN-KGKYHDKIPFPQPELASLGIKLLW---LGVVFGLP---LALGFSIPEVLICA 235
QY 331 -----FLLSHVVTNFNHYVEKFASSNMSNIAACLOIMTNNMRPGR-FID 375
Db 236 SVTYMTYGIIVCTIFMLAHVLESTEF-LTPDGESGAIDDEWAICQIRTNATNPNFWN 294
QY 376 WLKGLNLYQIEHHLFPPTPRHNLNTVMPVKFAAANGLPYVVDYFTGF-----WLE 428
Db 295 WFCGGLNQHNLHLPNTCHIHYPOLNIIKDVCOEFGVEYKVFYTFRAAIASNYRWLE 353

RESULT 6

S54809
linoleoyl-CoA desaturase (EC 1.14.99.25) - Spirulina platensis
N:Alternate names: Delta6-Desaturase
C:Species: Spirulina platensis
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997
C:Accession: S54809
R:Tasaka, I.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54809
A:Accession: S54809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <TAS>
A:Cross-references: EMBL:X87094; NID:g809109; PID:g809110
C:Keywords: oxidoreductase

Query Match 8.7% Score 211; DB 2; Length 368;
Best Local Similarity 24.3%; Pred. No. 6.3e-10;
Matches 90; Conservative 63; Mismatches 129; Indels 88; Gaps 21;
QY 111 LDRMRV----RAEGL--MDGSPFLFYIRKILETIFITILFAFYLOYHTYYP-----LP 154
Db 19 ELNRRVNAVLEAENISPRDNPPMY-----LKT--AILLAWVYSAWTFVVGPDVLMKIL 71
QY 155 SAILMGVAMQOQLGWLIIHEFAHQLFKNRYNDLASVFNGLQSSGGWKEQHN-VH 212
Db 72 GCIVLGFQVSAGVFNISHDGNGGYSKYQWNYLSG--LTHDAIGVSSYLKFRHNLVH 129
QY 213 AATNVVGRDGL--DLVPFVATVAEHLNNYSQDSWVNTLFRQHW--VHW--TFMLPFLR 265
Db 130 TYTNILGHDEVEHGDVLRMSPE-----YRWYHRYQHWFVYVYPIIP 174
QY 266 LSULL--OSIIFVSQMPHYDYRNTAIYEQVGLSLHW-AWSLQGLYFLPDWSTTRIM 321
Db 175 YWNSIADVQTMFLFRQ---YHDHEIPSPVTDIATLAFAGFVAVELIIP--IAGVY 227
QY 322 FLVSHLVGG-----FLLSHVVTNFNHYVEKFASSN--TMSNACLOIMTT 365
Db 228 SPLEAVIGASIVYVTHGLVACVWFLAHVI-----EPAEFLDPDNLHIDDEWAIACQVKT 282
QY 366 RNMPPGR-FIDWLWGLNLYQIEHHLFPPTPRHNLNTVMPVKFAAANGLPYVVDYFTG 424
Db 283 VDFAPNPNFIINWYVGLNLYQVTHLFPFHICHIHPKPIAPILAEVCEEFVNTAVHQTFFG 342
QY 425 -----FWLE 428
Db 343 ALAANYSLWK 352

RESULT 7
T07687
Omega-6 desaturase FAD2-1, microsomal - soybean
C:Species: Glycine max (soybean)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 26-Aug-1999
C:Accession: T07687
R:Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
Plant Physiol. 110, 311-319, 1996
A:Title: Developmental and growth temperature regulation of two different microsc
A:Reference number: Z16095
A:Accession: T07687
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-387 <HEP>
A:Cross-references: EMBL:L43920; NID:g904151; PID:g904152
A:Experimental source: seed
C:Genetics:
A:Gene: FAD2-1
C:Function:
A:Description: involved in production of polyunsaturated lipids; plays a major ro
A:Note: strongly expressed in developing seeds
C:Superfamily: omega-3 fatty acid desaturase

delta-6 fatty acid desaturase (EC 1.14.99.-) - human
C:Species: Homo sapiens (man)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #
C:Accession: T13155
R:Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
A:Title: Cloning, expression, and nutritional regula
A:Reference number: Z17612; MUID:9085046
A:Accession: T13155
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-444 <CHOS>
A:Cross-references: EMBL:AF126799; NID:g4405527; PID
C:Keywords: oxidoreductase

Query Match 15.4%; Score 374.5; DB 2; Length 444;
Best Local Similarity 26.5%; Pred. No. 3.1e-23;
Matches 118; Conservative 70; Mismatches 166; Indels 91; Gaps 17;

[illegible]

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RESULT      3
JG0180
delta-6 fatty acid desaturase (EC 1.14.99.-) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999
C:Accession: JG0180
R:AKI, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta
Biochem. Biophys. Res. Commun. 255, 575-579, 1999
A:Title: Molecular cloning and functional characterization of rat delta-6 f
A:Reference number: JG0180
A:Accession: JG0180
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-444 <AKI>
A:Cross-references: DDBJ:AB021980
C:Superfamily: cytochrome b5 core homology
C:Keywords: oxidoreductase
F:18-94/Domain: cytochrome b5 core homology <CB5>

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Query Match      15.1%; Score 367; DB 2; Length 444;
Best Local Similarity 25.1%; Pred. No. 1.3e-22;
Matches 123; Conservative 64; Mismatches 174; Indels 130; Gaps 17;

Qy 4 REQHERFFKIDGKWCQIDAVL-----RSHPGG-SAITTYKANMDATVTFHTFGSK 56
   | : : : | | : | | | | | | | | | | | | | | | | | | | | | | |
Db 22 RWESIQRHNLRTD-RWLVIDRKVYNTVQWQRHPGGRHVIGHYSGEDATDAFRAFLDLD 80
   | : : : | | : | | | | | | | | | | | | | | | | | | | | | | |

Qy 57 EAYOWLTELK-KECPTQEPPEIDKDDPIKIGDVNMGTFNISKRSAQINKSFDTLRMR 115
   | : : : | | : | | | | | | | | | | | | | | | | | | | | | | |
Db 81 FVGKFLAPLLIGELAPEP-----SLDRGKSSQITEDFRLAKKT 119
   | : : : | | : | | | | | | | | | | | | | | | | | | | | | | |

Qy 116 VRAEGLMDGSPFLVIRKILETIFTLFAFYL-QYHTYYLP----SAILMGVAAOOLGWL 170
   | : : : | | : | | | | | | | | | | | | | | | | | | | | | | |

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QY 171 HFAHQHQLFKRRYYNDLASFVGNFVQGGWKEQHNHVHAAATNVVGRDGLDLVPFY 230
    ! : ! : ! : ! : ! : ! : ! : ! : ! : ! : ! : ! : ! : ! : ! : ! : ! : ! : ! :
DB 180 HDYGHLSVYKKSINWHIVKHVEFVGHUHLKGASANWNNRHFQHAKPNIFHKDPDI 234
```

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Qy 231 ATVAEHLNNYSQDSWVMTLFRWQ-----HVHWTFML---PFLRLSWLLQS 272
      :      ||      ||      ||      ||      ||      ||
Db 234 -----KSLRVLVFWGOWPLEYGGKKLKYLPYNHQHEVFFLIGPPLL----- 275
      :      ||      ||      ||      ||      ||      ||
Qy 273 IIFVSMQPTHYDYRNATAYEQVGLSLHWAS-----LGQLYFLPDWST 317
      :      ||      ||      ||      ||      ||      ||
Db 275 -----IPMTFQYQIIMNRDDWDLAWAISYARFFYTPFFYIGILGALVFL----- 324
      :      ||      ||      ||      ||      ||      ||
Qy 318 RIMFFLVSH-LVGQFLSLHVV---TFNHYSEVKFALSSNMSVACLIQIMTRNMRPGRF 373
      :      ||      ||      ||      ||      ||      ||
Db 324 NFIRELESHFVWVYTMNHVIMEIDLHY-----RDWFESSOLAATCNVEQSFF 371
      :      ||      ||      ||      ||      ||      ||
Qy 374 IDWLWGLNGLVQIEHLEPPTMPRHNLNTVMPFLVKEFAAANGLPYMWDDYDFYGFWLEIQFR 433
      ||      ||      ||      ||      ||      ||      ||
Db 372 NDWFSGHNLVQIEHLEPPTMPRHNLHRIAPLVKSLCAKHGIEYQ-----EKPLLR 421
      :      ||      ||      ||      ||      ||      ||
Qy 434 NIANVAAKLTK 444
      :      ||      ||      ||
Db 422 ALLDIVSLKK 432

RESULT 4
T08765
probable Delta-6 fatty acid desaturase (EC 1.14.99.-) - human (fragment)
N:Alternate names: protein DKFZp586C201.1
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C:Accession: T08765
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A:Reference number: 216471

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A:Molecule type: mRNA
A:Residues: 1-311 <WAM>
A:Cross-references: EMBL:AL050118
A:Experimental source: adult uterus; clone DKFzp586C201
C:Genetics:
A:Note: DKFzp586C201.1
C:Keywords: oxidoreductase

Query Match          13.0%; Score 316.5; DB 2; Length 311;
Best Local Similarity 29.0%; Pred. No. 1.le-18;
Matches 87; Conservative 51; Mismatches 117; Indels 45; Gaps 10;

Qy 134 LEIT--PTILFAYLQVHTYLP---SAILMGVAMQOOLGWLIIHEFAHHQLFKRNYNDLA 188
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10 LESIANETV---FY-FGNQWIFTLATFATVLSQAQAGWLQHDYCHLSVYRKPKNNHLY 64
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 189 SYFGNPLQGFSSGGNKEQHNHHAATNVYGRDGDLDLPFYATVAEHLNLYSQDSNVMT 248
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-483-107

Query Match 10.0%; Score 243.448; DB 2; Length 911;
Best Local Similarity 27.6%; Pred. No. 6.6e-16;
Matches 21; Conservative 7; Mismatches 26; Indels 22; Gaps 5;
Qy 172 EPAHQLFKNRYNDLASVFGNFIQGFSSGGWKQ-----HNVHHAATNVVGRDGLDL 226
Db 691 EISH---FSNAYRNLIA-----FAEELSKNGTTGKNGYGHNAQNAKLGVNITAQDLDF 741
Qy 227 -----VPF--YATVA 234
Db 742 NGLMKRIPYGYATFA 757

RESULT 15
5223423-2
Patent No. 5223423
APPLICANT: FRANCHINI, GENOVEFFA; WONG-STAAL, FLOSSIE;
GALLO, ROBERT
TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/331,212
FILING DATE: 03-31-1989
SEQ ID NO: 2
LENGTH: 3077
5223423-2

Query Match 9.8%; Score 238.092; DB 5; Length 3077;
Best Local Similarity 19.8%; Pred. No. 1.3e-14;
Matches 33; Conservative 24; Mismatches 46; Indels 64; Gaps 11;
Qy 204 WKE-QHNVHHAATNVVGRDGLDLVPFYATVAEHLNNYSQDSWVMTLFRWQ-HVHWTFML 261
Db 2548 QWEWEHKIRFLEANI---SESL-----QAQIQEKNMVE---LQKLSNDVDFGNW---- 2593
Qy 262 PFLRLSWL-----LQSIIFVSQMPHYDYRNTAI-----Y 293
Db 2593 -FDUTSWIKYIQGYMIVGVIVALRIVIVVQMLSLRLKRGYRPSVSLPPGYIQIHIHKDW 2651

Qy 294 EQ-----VGLSLHNAWSILGQLYFLPDKSTRIMFVLVSHL 327
Db 2652 EQPDREETEEDVGNVDVG-SRSWPPPIEYIHFL-----IRLLIRLLTRL 2693
Search completed: February 25, 2000, 00:29:31
Job time: 25089 sec

RESULT 12

US-08-337-483-5

; Sequence 5, Application US/08337483

; Patent No. 5922562

; GENERAL INFORMATION:

; APPLICANT: Loosmore, Sheena

; APPLICANT: Harkness, Robin

; APPLICANT: Schryvers, Anthony

; APPLICANT: Chong, Pele

; APPLICANT: Gray-Owen, Scott

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Murdin, Andrew

; APPLICANT: Klein, Michel

; TITLE OF INVENTION: Transferrin Receptor Genes

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sim & McBurney

; STREET: Suite 701, 330 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5G 1R7

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/337,483

; FILING DATE: 08-NOV-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Stewart, Michael I

; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb

; TELEPHONE: (416) 595-1155

; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 913 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-337-483-5

Query Match

Best Local Similarity 24.1%; Score 243.52; DB 2; Length 913;

Matches 28; Conservative 20; Mismatches 45; Indels 23; Gaps 7;

Qy 375 SHLVGGFLLSHVTFNHYSVKFAALSSNMSYACIQINTTRMRPGRFIDWLWGLNLYQ 384

Db 550 AELVGGDLNCGKSSNSDCKVRLKG--KNY---YFAARNMALGKIYD-LGLGMRYD 603

Qy 385 IEHHLFTPMRHNLTN-MPLVKEFAAANGLPYVDDYFTGFWEIEQ-----FRN 434

Db 604 V-----SRTKANESTISVGKFNFSWNTGIVIKTE-----WLDLSYRLSTGFEN 648

RESULT 13

US-08-478-435-107

; Sequence 107, Application US/08478435

; Patent No. 5922323

; GENERAL INFORMATION:

; APPLICANT: Loosmore, Sheena

; APPLICANT: Harkness, Robin

; APPLICANT: Schryvers, Anthony

; APPLICANT: Chong, Pele

; APPLICANT: Gray-Owen, Scott

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Murdin, Andrew

; APPLICANT: Klein, Michel

; TITLE OF INVENTION: Transferrin Receptor Genes

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sim & McBurney

; STREET: Suite 701, 330 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5G 1R7

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/478,435

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/337,483

; FILING DATE: 08-NOV-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/175,116

; FILING DATE: 29-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/148,968

; FILING DATE: 08-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Stewart, Michael I

; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg

; TELEPHONE: (416) 595-1155

; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 107:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 911 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-478-435-107

Query Match

Best Local Similarity 27.6%; Score 243.448; DB 2; Length 911;

Matches 21; Conservative 7; Mismatches 26; Indels 22; Gaps 5;

Qy 172 EFAHQHQLFKNRYNDLASYFVGNFLQGFSSGGWKQ-----HNVHAATNVYGRGDDL 226

Db 691 EISH---FSNAYRNLI-----FAEELSKNGTGTGKNGYHNAQNAKLVGVNITQLDF 741

Qy 227 -----VPF--YATVA 234

Db 742 NGLWKRIPIGWYATFA 757

RESULT 14

US-08-337-483-107

; Sequence 107, Application US/08337483

; Patent No. 5922562

; GENERAL INFORMATION:

; APPLICANT: Loosmore, Sheena

; APPLICANT: Harkness, Robin

; APPLICANT: Schryvers, Anthony

; APPLICANT: Chong, Pele

; APPLICANT: Gray-Owen, Scott

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Murdin, Andrew

; APPLICANT: Klein, Michel

; TITLE OF INVENTION: Transferrin Receptor Genes

5187091-2
LENGTH: 652

Query Match 10.4%; Score 253.184; DB 5; Length 652;
Best Local Similarity 18.1%; Pred. No. 4.3e-17;
Matches 98; Conservative 68; Mismatches 190; Indels 185; Gaps 22;

QY 31 PGSSAITTKNMDATTVEHFFHGSKEAYOW-----LTELKKECPQEPEDIK- 81
DB 83 PRGALTSFVOSLNTIW-----PSDADPWKAFMAQVEVLIDKKIEEYAKSKALAELOQ 136
QY 81 -----DDPIKIGIDVANGTFNISEKSA-QINKSFIDLRMRVRAEGLMDGSPFLYIRKIL 134
DB 137 LQNNFEDYVNALNSWKKTPLSLRSKRSQDRIRLEFSQAESHR-----NSMPSFAVSK-F 190
QY 135 ERIFTILFAYLOYHTYTPSAILMGVAMQOLGWLHFEFAHOLFKNRYND--LASIFY 192
DB 191 EYLFPTYAQAANTHLLLLKDAQVGEEMGYSSDVAEFHROLKLTQVTDHCVNWNV 250
QY 193 G-NFQGFSSGGKQHNHHAATNVVGRDGLDLV---PFYATVAEHLNNYSQDSWVMT 248
DB 251 GUNGLGSGTYDAWVFNFRREMTLV-----LDLVLFPFY-----DIRLSKG----- 296
QY 249 LFRQHVHWTMLPFLRLSLW-----LQSIIFVSOMPTHY--- 284
DB 296 -VKTELTRDIFDPIFSLATLOEYGTFLSIENSIRKPHLDYLOQIEFTRLQPGYFK 354
QY 284 -DYIRNT-----AYEQVGLSLHWASL 306
DB 355 DSFNWNGNYVETRPISGSKTITSPFYGDKSTEPVQKLSFDGQKVRTIANTDVAAPN 414
QY 307 GOLYFLPDWSTRIMFLVSHLVGGFLLSHVTFNHYSVKEFALSSNIMS----- 356
DB 415 GRVY-----LGVTKYDFSQDDQKNTSTQTYDSKRNNHVSQAQ 453
QY 356 -----NYA-CLQIMTTRNMRPGRFIDWLWGLNLYOIEHHLFP 391
DB 454 DSIDQLPPTTDEPLEKAYSHOLNVAECFLMDRRGTIP--FTWTHRSVDF-----FN 505
QY 392 TMRNRLNTVPLVKEFAAANGLPMVDDYFTGFWL-----EIOFRNTANVAAKLT 443
DB 506 TIDAEKI-TOLPVKAYALSSGASIEGPGFTGNNLLFKESSNIAKFKVTLNSAALLQ 564
QY 444 K 444
DB 565 R 565

RESULT 10
5223423-4

Patent No. 5223423
APPLICANT: FRANCHINT, GENOVEFFA,WONG-STAAAL, FLOSSIE;
GALLO, ROBERT
TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/331,212
FILING DATE: 03-31-1989
SEQ ID NO:4
LENGTH: 3080

5223423-4

Query Match 10.4%; Score 253.124; DB 5; Length 3080;
Best Local Similarity 22.4%; Pred. No. 4.1e-16;
Matches 15; Conservative 14; Mismatches 23; Indels 15; Gaps 3;

QY 271 QSIIFVSOMPTHYDYVNTAIYEQVGLSLHWANSLGOLYFLPDWS-----TRIMEFL 323
DB 1143 EALVINGRIPKFLHLPVERET--WEO-----WWDNVQVWTIPDQWDFVSTPLVRLAFNL 1194

QY 324 VSHLVGG 330
DB 1195 VKDPIPG 1201

RESULT 11

US-08-478-435-5
Sequence 5, Application US/08478435
Patent No. 5922323
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESS: Sim & McBurney,
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-435-5

Query Match 10.0%; Score 243.52; DB 2; Length 913;
Best Local Similarity 24.1%; Pred. No. 6.5e-16;
Matches 28; Conservative 20; Mismatches 45; Indels 23; Gaps 7;

QY 325 SHLVGGFLLSHVTFNHYSVKEFALSSNINSVACLOIMTRNMRPGRFIDWLWGLNLYQ 384
DB 550 AELVGGDLCKYQKSSNICKVRLKIG--KNY---YFAARNNALGKYVD-LGLGMRDY 603
QY 385 IEHLLFTMPRHLNLTVMPLVKEFAAANGLPYMVDDYFTGFWEIQO-----FRN 434
DB 604 V-----SRKANEISISVCKFKNFSTGIVIKPTE-----WLDLSYRLSTGFRN 648

```

; TITLE OF INVENTION:  OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANT
; NUMBER OF SEQUENCES:  18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  RAE-VENTER LAW GROUP, P.C.
; STREET:  260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY:  PALO ALTO
; STATE:  CA
; COUNTRY:  USA
; ZIP:  94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/834.655
; FILING DATE:  11-APR-1997
; CLASSIFICATION:  435
; ATTORNEY/AGENT INFORMATION:
; NAME:  RAE-VENTER, BARBARA
; REGISTRATION NUMBER:  32,750
; REFERENCE/DOCKET NUMBER:  CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (650) 328-4400
; TELEFAX:  (650) 328-4477
; TELEX:  N/A
; INFORMATION FOR SEQ ID NO:  7:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  252 amino acids
; TYPE:  amino acid
; STRANDEDNESS:  not relevant
; TOPOLOGY:  linear
; MOLECULE TYPE:  peptide
; US-08-834-655-7

Query Match      10.7%; Score 259.5; DB 2; Length 252;
Best Local Similarity 25.5%; Pred.No.2.5e-18;
Matches 63; Conservative 49; Mismatches 110; Indels 25; Gaps 5

Qy  155 SAILMGVAMQQLGWLHIEFAHHOLFKNRYNDLASFYVGNFLQGSSGGWKEOHNVHAA 214
    :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db  18 AALGLLWIOASAYIGHDSGHYVIMNSKSYNRFALLSGNCILTGISIAWKWTHNAHLA 77
    :|::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy  215 TNYVGROGDLDLPFYATVAEHLNNYSQDSW-----VMTLFRWQHVVHTFMPLPFLR 265
    :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db  78 CNSLDYDPDLQHIPPVFAYSTFEFFSLTSREYDRKLTFGPVARELVSYQHFTYYPVNCFGR 137
    :|::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy  266 LSWLLQSITFY--SQMPTHYDYIYRNTAIYEQVGLSLHWANSLGOLYLPLDWTIMFF 322
    :::||::||::||::||::||::||::||::||::||::||::||::||::||
Db  138 INFLEQTELLFSKREVDPDALNF-----AGILVEVTWFPLLVSCLPNWPERRFFV 188
    :|::||::||::||::||::||::||::||::||::||::||::||::||

Qy  323 LVSHLVGGFLLSHV-VTNHNHSVEKFALESSNTMSNYACLOIWTTRNMRRGCRFDLWGGL 381
    ||::||::||::||::||::||::||::||::||::||::||::||::||
Db  189 FTSETVTA--LQHIQTLLNHFAADYV-YGPPTGSDWFEXQAAGTIDISCRSYMDFEGGL 245
    :|::||::||::||::||::||::||::||::||::||::||::||::||

Qy  382 NYQIEHH 388
    :|::||::||::||::||::||::||::||::||::||::||::||::||
Db  246 QFQLEHH 252
    :|::||::||::||::||::||::||::||::||::||::||::||::||

RESULT          9
5187091-2
; Patent No. 5187091
; APPLICANT: DONOVAN, WILLIAM P.; RUPAR, MARK J.; SLANEY,
; ANNETTE C.; JOHNSON, TIMOTHY B.
; TITLE OF INVENTION: BAGILLUS THURINGIENSIS CRYIIIC GENE
; . ENCODING TOXIC TO COLEOPTERAN INSECTS
; NUMBER OF SEQUENCES:  2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/07/496.568
; FILING DATE:  20-MAR-1990
; SEQ ID NO.:2

```

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,779
 FILING DATE: 30-DEC-1994
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 83832YXW
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-366-779-5

Query Match 16.6%; Score 403.5; DB 1; Length 448;
 Best Local Similarity 27.0%; Pred. No. 2.1e-32;
 Matches 123; Conservative 69; Mismatches 199; Indels 65; Gaps 16;

QY 12 FIKIDGKWCDDAVLRSHPGGS-AITTYKNMDATTVFHTHTGSKAYQMLTELKKECP 70
 DB 24 WISIOGRAYDVSDWV-KDHFGGSPPLKSLAGQEVTDFAVAFHPAS-----TW----- 70
 QY 71 TOPEIPDIKDDPIKIDGDDVNMGTFNISERSAQINKSFDTLRMRVRAEGLMDG----- 125
 DB 70 -----KNLDKFFTG-YILKDYSVSEVSKDYRKLVFEFSKMGLYDKKHIMF 114
 QY 125 SPLFYIRKILE-TITFILFAFYLOYHTYILPSAILMGVAMQQLGWLIEFAHQLFKNRY 183
 DB 115 ATLCFIAMLFAMSVYGLFCEGVLVHLF---SGCLMGFLWTQSGWIGHDAGHYMVVSDSR 171
 QY 184 YNDLASVFGNFGLOGSSGQKQHNHHAATNVVGRDGLDLP-----FYATVAEH 236
 DB 172 LNFEMGIFAANCLSGISIGWKNWNAHHAACNSLEYDPPDQYIPFLVSSKFFGSLTS 231
 QY 237 L--NNYSQDSWMVTLFRQVHWTFF--MLPFLRLSLLQSIIFVSQMPHTHYDYRNTA- 292
 DB 232 FYEKRLTFDS--LSRFFVSQHTWTFYIPMCAARLNNYVQSLIMLLTK-----RVNSY 281
 QY 292 -IYEQVGLSHWANSGLQLYFLPDWSTRIMFFLVSHLVGGLSHVVTNFHYSVEKFA 350
 DB 282 RAQELGLCLVFSIWYPLLVSCLPNMGIRIMFVIASLSVTG-MQOVQFSLNHFSSVY-VG 339
 QY 351 SNIMSNYACLOIMTTRNMRPGREFIDWGLNQLVQIEHHLFPTMPRHNLNTVMPLVKEFAA 410
 DB 340 KPGKNWFEKQDGTDLDISCPPMDFHGGSGQFQIEHHLFPKMPRCNLRKISPYIELCK 399
 QY 411 ANGLPYMVDYFTGFWEIEQFRNIANVAALKTKKI 446
 DB 400 KHNLPYNASFSKANEMTLTLNTALQARDITKPL 435

RESULT 6

US-08-789-936-5
 Sequence 5, Application US/08789936
 Patent No. 5789220
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 APPLICANT: Reddy, Avutu S.
 APPLICANT: Nuccio, Michael
 APPLICANT: Freyssinet, Georges L.
 APPLICANT: Nunberg, Andrew N.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/789,936
 FILING DATE: 28-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/366,779
 FILING DATE: 30-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 83832YXW
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE:
 US-08-789-936-5

Query Match 16.6%; Score 403.5; DB 1; Length 448;
 Best Local Similarity 27.0%; Pred. No. 2.1e-32;
 Matches 123; Conservative 69; Mismatches 199; Indels 65; Gaps 16;

QY 12 FIKIDGKWCDDAVLRSHPGGS-AITTYKNMDATTVFHTHTGSKAYQMLTELKKECP 70
 DB 24 WISIOGRAYDVSDWV-KDHFGGSPPLKSLAGQEVTDFAVAFHPAS-----TW----- 70
 QY 71 TOPEIPDIKDDPIKIDGDDVNMGTFNISERSAQINKSFDTLRMRVRAEGLMDG----- 125
 DB 70 -----KNLDKFFTG-YILKDYSVSEVSKDYRKLVFEFSKMGLYDKKHIMF 114
 QY 125 SPLFYIRKILE-TITFILFAFYLOYHTYILPSAILMGVAMQQLGWLIEFAHQLFKNRY 183
 DB 115 ATLCFIAMLFAMSVYGLFCEGVLVHLF---SGCLMGFLWTQSGWIGHDAGHYMVVSDSR 171
 QY 184 YNDLASVFGNFGLOGSSGQKQHNHHAATNVVGRDGLDLP-----FYATVAEH 236
 DB 172 LNFEMGIFAANCLSGISIGWKNWNAHHAACNSLEYDPPDQYIPFLVSSKFFGSLTS 231
 QY 237 L--NNYSQDSWMVTLFRQVHWTFF--MLPFLRLSLLQSIIFVSQMPHTHYDYRNTA- 292
 DB 232 FYEKRLTFDS--LSRFFVSQHTWTFYIPMCAARLNNYVQSLIMLLTK-----RVNSY 281
 QY 292 -IYEQVGLSHWANSGLQLYFLPDWSTRIMFFLVSHLVGGLSHVVTNFHYSVEKFA 350
 DB 282 RAQELGLCLVFSIWYPLLVSCLPNMGIRIMFVIASLSVTG-MQOVQFSLNHFSSVY-VG 339
 QY 351 SNIMSNYACLOIMTTRNMRPGREFIDWGLNQLVQIEHHLFPTMPRHNLNTVMPLVKEFAA 410
 DB 340 KPGKNWFEKQDGTDLDISCPPMDFHGGSGQFQIEHHLFPKMPRCNLRKISPYIELCK 399
 QY 411 ANGLPYMVDYFTGFWEIEQFRNIANVAALKTKKI 446
 DB 400 KHNLPYNASFSKANEMTLTLNTALQARDITKPL 435

TELEFAX: (650) 328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 355 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-5

Query Match 22.88; Score 555; DB 2; Length 355;

Best Local Similarity 34.58; Pred. No. 9.8e-48;
 Matches 124; Conservative 65; Mismatches 134; Indels 36; Gaps 8;

QY 112 LRMVRAEGLMDGSPLEFIRKI-----LETITLILFAYLYHY-YLPSSAILMGVAMQ 165
 DB 5 LRTLFQSLGYDSSKAYAFKVSFNLCTWGLSTIVAKWGTSTLANVLSAALLGLFWQ 64
 QY 166 LGWLIHEFAHQLPKRYNDLASFYVGNFLOGFSSGGWKEQHNHHAATNVVGRDGLD 225
 DB 65 CGWLADFLHQVQDFRFGDLFLGAGVCGQFSSSSWKKDNTTHAAPNVHGEDPDID 124
 QY 226 LVFAYATVAEHLNYSOD-----SWMTLFRWQHVTFF--MLPELRLSLWLLQSIIFV- 277
 DB 125 THPL-LTWSEHALEMFSDVDEELTRMSRFWLNQWTFYFPLISFAKLSWCLQSILFVL 183
 QY 277 -----SOMPTHYDYRYNTAIYEQVGLSLHAWSLGQLY-FLPDWSTRIMEFLVS 325
 DB 184 PNGAHPKSGARVP-----ISLVEQLSLAMHTWYLATMFLFKIDPNVLMVYFLVS 234
 QY 326 HLVGGLLSHYVTNHYNSVEKFASSNIMSNYACLIQMTTRNMRPGRFIDMLWGLNLYQI 385
 DB 235 QAVCGNLLAIVSLNHNMPVISEEAVDMDFETKQIITGRDVHPGLFANFTGLNLYQI 294
 QY 386 EHLFPMPRHNLNTVPLVKEFAAAGLPPYVDDYFTGFWELEIOFRNIANVAALTK 444
 DB 295 EHLFPMPRHNLNTVPLVKEFAAAGLPPYVDDYFTGFWELEIOFRNIANVAALTK 444

RESULT 4

US-08-833-610-5
 ; Sequence 5, Application US/08833610
 ; Patent No. 5972664
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUTZON, DEBORAH
 ; APPLICANT: MURKERT, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 ; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833.610
 ; FILING DATE: 11-APR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: CGNE.123.000S
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)328-4400
 TELEFAX: (650)328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 446 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-833-610-5

Query Match 16.74; Score 407.5; DB 2; Length 446;

Best Local Similarity 27.24; Pred. No. 8.3e-33;
 Matches 124; Conservative 69; Mismatches 198; Indels 65; Gaps 16;

QY 12 FIKDGGKQICDDAVLRSHPGGS-AITYKNMDATTVFHTFTGTSKEAYQMLTELKKECP 70
 DB 24 WISIOGRAYDVSDWV-KDHPPGSPPLKSLAGQEVTDFAVAFHPS-----TW----- 70
 QY 71 TOPEIPIKDDPIKIGIDDDVNMGTENISEKRSQAQINKSFTDLRMVRAEGLMDG----- 125
 DB 70 -----KNLDKFTG-YLKDYSVSEVSKYKLVFEFSKMGLYDKKGHIMF 114
 QY 125 SPLPYIRKILB-TITLILFAYLYHYLPSSAILMGVAMQOOLGWLHIEFAHQLPKRY 183
 DB 115 ATLCFIAMLFAMSYGVLFCEGLVHLF---SGCLMGFLWQSGWIGHDAGHYMVVSDSR 171
 QY 184 YNDIASFVGNFLOGFSSGGWKEQHNHHAATNVVGRDGLDLP-----FYATVAEH 236
 DB 172 LNKFMGIFAACLSGISIGMWNHNAHIAACNSLEYDPLQYIPFLVSSKFGSLTSH 231
 QY 237 L--NNYSQDSVMTLFRWQHVTFF--MLPELRLSLWLLQSIIFYSQMPTHYDYRYNTA- 292
 DB 232 FYERKLIFDS--LSRFYSYQHTFYFIMCAARLNMVQSLIMLLTK-----RNVSY 281
 QY 292 -IYQVGLSLHAWSLGQLYFLPDWSTRIMEFLVSHLVGGFLLSHVVTFNHYNSVEKFA 350
 DB 282 RAQELGLCLVSIWYPLLVSCLPNKGRIEVIASLVTG-MQOVQFSLNHFSSVY-VG 339
 QY 351 SNIMSNYACLIQMTTRNMRPGRFIDMLWGLNLYQIEHLLFTMPRHNLNTVPLVKEFA 410
 DB 340 KPGNNMFKEQTDGTLDISCPWDMFHHGQFQIEHLLFPMPRCNRKISPIYIELCK 399
 QY 411 ANGLPYVDDYFTGFWELEIOFRNIANVAALTKKI 446
 DB 400 KHNLPYVASFPSKANWTLRLTNALQARDITKPL 435

RESULT 5

US-08-366-779-5
 ; Sequence 5, Application US/08366779
 ; Patent No. 5614393
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freyssinet, Georges L.
 ; APPLICANT: Nundberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:

Db 80 LANFYVGDIDSDRDIKNDDF-----AAEVRK-----LRTLFQSLGYD 118
Qy 124 GSPFLFYIRKI-----LETIFTILFAFYLOVHTY-YLPSAILMGVANOQGLWLIHEFAHQ 177
Db 119 SSKAYAFKVSFNLCTWGLSTVIVAKWGTSTLANVLSAALLGLFWOQCGWLAHDFLHQ 178
Qy 178 LFKNRYNDLASFYVGNFLQFSGGKKEOHNVHHAATNVVGRDGLDLVPPFYATVAEHL 237
Db 179 VFQDRFWGLFGAFLGVCQGFSSWKKHNTTHAAPNVHGEDPIDHTPL-LTWSEHA 237
Qy 238 NNYSD-----SWMTLFRQHVHTF--MLPFLRLSWLQSIIFV-----SQ 278
Db 238 LEMFSDVPDEELTRMWSRFVNLQTFYFPLISFARLSWCLOSILEVLPNGOAHKPSGAR 297
Qy 279 MPTHYDYRNTAIYEQVGLSLHNAWSLGOLY-FLPDWSTRTIMFFLVSHVGLLSHVY 337
Db 298 VP-----ISLVEQLSLAMHTWYLATMFLFKDPVNMVLYFLVSOAVCGNLLAIVF 348
Qy 338 TFNHYVSEKFASSNIMSACLOIMTRMRPGRFIDWLWGLNYQIEHHLFPTMPRHN 397
Db 349 SLNHNMGMPVISKEEAVIDMDFTKQITGRDVHPGLFANFTGGLNYQIEHHLFPTMPRHN 408
Qy 398 LNTVMPLYKEFAAANGLPYVDDYFTGFWELEIQFRNIANVAALKTK 444
Db 409 FSKIOPAVETLCKKYNRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 2

US-08-833-610-4
; Sequence 4, Application US/08833610
; Patent No. 5972664
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,610
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.123.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)328-4400
; TELEFAX: (650)328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-833-610-4

Query Match 25.5%; Score 620; DB 2; Length 457;
Best Local Similarity 32.8%; Pred. No. 4.3e-54;
Matches 153; Conservative 76; Mismatches 176; Indels 62; Gaps 13;

Qy 4 REQHEPFIKIDGKCQIDDAVLSRSHPGGSAITTKNNKDATYVFTFTHTGSKAEQWLT 63
Db 25 KDAEAPFMIIDNKVYDVEEV-PDHPGGSVILTHVGKDGTDVDFTH---PEA-AWET 79
Qy 64 ELKKECPTPEIPDIKDDPIKIGIDVNVNGTENISEKRSQAQINKSTDLRMRVRAEGLMD 123
Db 80 LANFYVGDIDSDRDIKNDDF-----AAEVRK-----LRTLFQSLGYD 118
Qy 124 GSPFLFYIRKI-----LETIFTILFAFYLOVHTY-YLPSAILMGVANOQGLWLIHEFAHQ 177
Db 119 SSKAYAFKVSFNLCTWGLSTVIVAKWGTSTLANVLSAALLGLFWOQCGWLAHDFLHQ 178
Qy 178 LFKNRYNDLASFYVGNFLQFSGGKKEOHNVHHAATNVVGRDGLDLVPPFYATVAEHL 237
Db 179 VFQDRFWGLFGAFLGVCQGFSSWKKHNTTHAAPNVHGEDPIDHTPL-LTWSEHA 237
Qy 238 NNYSD-----SWMTLFRQHVHTF--MLPFLRLSWLQSIIFV-----SQ 278
Db 238 LEMFSDVPDEELTRMWSRFVNLQTFYFPLISFARLSWCLOSILEVLPNGOAHKPSGAR 297
Qy 279 MPTHYDYRNTAIYEQVGLSLHNAWSLGOLY-FLPDWSTRTIMFFLVSHVGLLSHVY 337
Db 298 VP-----ISLVEQLSLAMHTWYLATMFLFKDPVNMVLYFLVSOAVCGNLLAIVF 348
Qy 338 TFNHYVSEKFASSNIMSACLOIMTRMRPGRFIDWLWGLNYQIEHHLFPTMPRHN 397
Db 349 SLNHNMGMPVISKEEAVIDMDFTKQITGRDVHPGLFANFTGGLNYQIEHHLFPTMPRHN 408
Qy 398 LNTVMPLYKEFAAANGLPYVDDYFTGFWELEIQFRNIANVAALKTK 444
Db 409 FSKIOPAVETLCKKYNRYHTTGMIEGTAEVFSRLNEVSKAASKMGK 455

RESULT 3

US-08-834-655-5
; Sequence 5, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400

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OM protein - protein search, using sw model

Run on: February 24, 2000, 17:31:22 ; Search time 16.6 Seconds
(without alignments)
358.072 Million cell updates/sec

Title: PCT-US99-28655-2

Perfect score: 2435
Sequence: 1 MYLREQEHEFFIKDKWC.....EIQFRNIANVAALKYKIA 447

Scoring table: BLOSUM62

Searched: 133990 seqs, 13297546 residues

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Word size: 0

Number of hits that pass the threshold : 133990
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/PGTUS9.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629	25.8	457	2	US-08-834-655-2
2	620	25.5	457	2	US-08-833-610-4
3	555	22.8	355	2	US-08-834-655-5
4	407.5	16.7	446	2	US-08-833-610-5
5	403.5	16.6	448	1	US-08-366-779-5
6	403.5	16.6	448	1	US-08-789-936-5
7	284.5	11.7	87	2	US-08-834-655-10
8	259.5	10.7	252	2	US-08-834-655-7
9	253.184	10.4	652	5	5187091-2
10	253.124	10.4	3080	5	523423-4
11	243.52	10.0	913	2	US-08-478-435-5
12	243.52	10.0	913	2	US-08-337-483-5
13	243.448	10.0	911	2	US-08-478-435-107
14	243.448	10.0	911	2	US-08-337-483-107
15	238.092	9.8	3077	5	523423-2
16	237.02	9.7	1648	2	US-08-662-227-35
17	232.872	9.6	1365	5	5194600-4
18	231.368	9.5	914	2	US-08-478-435-11
19	231.368	9.5	914	2	US-08-337-483-11
20	230.5	9.5	445	2	US-08-833-610-2
21	229.12	9.4	1165	5	5188960-4
22	227.388	9.3	1280	5	5206352-4
23	227.352	9.3	1286	5	5206163-1
24	227.096	9.3	1333	2	US-08-662-227-34
25	227.012	9.3	1642	2	US-08-662-227-2
26	226.248	9.3	2615	5	5206163-3
27	224.592	9.2	912	2	US-08-478-435-7
28	224.592	9.2	912	2	US-08-478-435-9
29	224.592	9.2	912	2	US-08-337-483-7
30	224.592	9.2	912	2	US-08-337-483-9
31	222.212	9.1	1179	5	5188960-2
32	220.584	9.1	845	5	5196194-17
33	218.416	9.0	3025	5	523423-3
34	214.312	8.8	1174	5	5188960-8

35 214.092 8.8 1189 5 5188960-6
36 214.032 8.8 2894 2 US-08-391-671A-23
37 213.268 8.8 919 2 US-08-788-674-4
38 212.772 8.7 751 5 5220013-2
39 212.168 8.7 908 2 US-08-478-435-94
40 212.168 8.7 908 2 US-08-337-483-94
41 211.072 8.7 952 2 US-08-788-674-5
42 211.211 8.7 359 1 US-08-307-382-2
43 211 8.7 359 1 US-08-366-779-2
44 211 8.7 359 1 US-08-478-727-2
45 211 8.7 359 1 US-08-473-508-2

ALIGNMENTS

RESULT 1
US-08-834-655-2
; Sequence 2, Application US/08834655
; Patent No. 5958809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-834-655-2

Query Match 25.8%; Score 629; DB 2; Length 457;
Best Local Similarity 33.0%; Pred. No. 5.4e-55;
Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;
Qy 4 REQEHEFFIKDKWCQIDDAVLRSHPGGSIAITTYKNMDATVTHHTGSKRAYOWILT 63
Db 25 KDAEAPFLMIIDNKVYDVREFV-PDHPGGSVILTHVGKDGDFDFTFH---PEA-AWET 79
Qy 64 ELKKECPQEPPEIPDKDDPKIGIDVNGVFNISEKSAQINKSFDTLRLMRVRAEGLMD 123

PS Example 2: Pages 105-106; 165pp; English.
CC The present sequence represents a peptide derived from a desaturase
CC enzyme. The specification describes methods for desaturating a
CC fatty acid and for producing a desaturated fatty acid by expressing
CC increased levels of a desaturase. Desaturases can be used for
CC desaturating fatty acids. The enzymes can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
CC cancer, diabetes or eczema or reduce blood pressure. They can also be
CC used to inhibit platelet aggregation, cause vasodilation, lower
CC cholesterol levels, inhibit proliferation of vessel wall smooth muscle
CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
CC other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
CC multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
SQ Sequence 87 AA;

Query Match 11.7%; Score 284.5; DB 1; Length 87;
Best Local Similarity 67.9%; Pred. No. 3.8e-22;
Matches 53; Conservative 7; Mismatches 17; Indels 1; Gaps 1;
QY 365 TRNRRGRFTDNLWGLNYQIEHLLFTMPRHNLNTVMPLVKFAAANGLPYMYDDYFTG 424
Db 8 TRNTPSPFTDNLWGLNYQIEHLLFTMPRHNLNTVMPLVKFAAANGLPYMYDDYFTG 424
QY 425 FWLEIEQFRNIAN-VAAK 441
Db 68 YNLNLOOLKNMAELVQAK 85

Search completed: February 25, 2000, 04:45:46
Job time: 23781 sec

QY 153 LPSAILMGVAMQOLGLWLFHFAHQLFKNRYINDLASVFNFLQFSSGGKQEHNVHH 212
 DB 12 LITAFVLTSAQAGWLOHGYCHLSVYRKPKNHLVHFKVIGHLKAGASANNWHRHFOHH 71
 QY 213 AATNVYGRDGLDLPVFFATVAEHLNNYSQDSWVMTLFRQVHVTMFLPFLRLSLWLLQS 272
 DB 72 AKPNIFHKDPDVMNHLVFLGEMQPIEYKGLKLYLPYNHQHEFFLIGPPLLPIMYFOY 131
 QY 273 IIFVQMPHYDYRNTAIYEQVGLSLHWASLQGLYFLPDWSTRIIMFFLVSHLVGG-- 331
 DB 132 QIIM-----TMVHKNNVDLAWAYS---YYIRFFITYIPFY---GILGALL 171
 QY 331 -----FLLSH---VVTFNHYSVEKFASSNIMSNYACLOQIMTTRNMRPGRFIDWLWGG 380
 DB 172 FLNTRFLESWHFVWVQTNHIVME---IDQAYRDWFSQLTATCNVEQSFENDWFSGH 228
 QY 381 LNYQIEHHLFTPMRHNLTVMPLVKEFAAANGLPY 416
 DB 229 LNFQIEHHLFTPMRHNLTVMPLVKEFAAANGLPY 264

RESULT 14

W95513
 ID W95513 standard; Protein: 615 AA.
 AC W95513;
 DE 26-MAR-1999 (first entry)
 KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
 KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
 KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
 KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
 KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
 KW diabetes; cosmetic; animal feed; human.
 OS Homo sapiens.
 FH Key
 FT Misc_difference 295 /note= "encoded by TGA"
 FT Misc_difference 321 /note= "encoded by TGA"
 FT Misc_difference 458 /note= "encoded by TGA"
 FT Misc_difference 491 /note= "encoded by TGA"
 FT Misc_difference 517 /note= "encoded by TAA"
 FT Misc_difference 535 /note= "encoded by TAG"
 FT Misc_difference 550 /note= "encoded by TGA"
 FT Misc_difference 615 /note= "encoded by TGA"
 FT Misc_difference /note= "encoded by TG"
 PN W09846764-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07421.
 PR 24-OCT-1997; US-956985.
 PR 11-APR-1997; US-833610.
 PR 11-APR-1997; US-834033.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P,
 PI Thurmond J;
 PI WPI: 99-080739/07.
 DR N-PSDB: X00909.
 PT Nucleic acid construct able to express fatty acid desaturase in
 PT plants - useful in human or animal nutrition, as cosmetics and
 PT therapeutically, e.g. for restenosis, cancer and diabetes
 PS Claim 48: Page 167-169: 210pp; English.
 CC The invention relates to a nucleic acid construct that contains at least
 CC one of the nucleotide sequences (X00899 to X00891) encoding Mortierella
 CC alpina delta 6, delta 12 and delta 5 desaturases (W95504 to W95506)
 CC respectively, coupled to an expression control sequence functional in

CC plants. Recombinant plant cells containing at least one DNA encoding a
 CC M. alpina fatty acid desaturase (FAD), can be used for the production of
 CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants
 CC containing them are used to produce oils such as linoleic acid,
 CC arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic acid,
 CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
 CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
 CC dietary supplements or substitutes, for use in humans or animals; (iii)
 CC for treating disorders associated with inadequate consumption or
 CC production of PUFA (or their metabolites such as prostaglandins), e.g.
 CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
 CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
 CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
 CC related coding sequences. Recombinant plants can produce high yields of
 CC PUFA, since new pathways can be created and unwanted ones suppressed.
 CC Plants can be engineered to express oils of particular PUFA composition,
 CC e.g. one similar to that in human milk, and product recovery is simpler
 CC than with e.g. fish. Sequences W95508-514 represent amino acid sequences
 CC of various contigs of human desaturase genes which are similar to the
 CC M. alpina desaturase sequences.
 SQ Sequence 615 AA;

Query Match 12.8%; Score 312.5; DB 1; Length 615;
 Best Local Similarity 29.0%; Pred. No. 8.9e-24;
 Matches 80; Conservative 46; Mismatches 115; Indels 35; Gaps 6;
 QY 153 LPSAILMGVAMQOLGLWLFHFAHQLFKNRYINDLASVFNFLQFSSGGKQEHNVHH 212
 DB 12 LITAFVLTSAQAGWLOHGYCHLSVYRKPKNHLVHFKVIGHLKAGASANNWHRHFOHH 71
 QY 213 AATNVYGRDGLDLPVFFATVAEHLNNYSQDSWVMTLFRQVHVTMFLPFLRLSLWLLQS 272
 DB 72 AKPNIFHKDPDVMNHLVFLGEMQPIEYKGLKLYLPYNHQHEFFLIGPPLLPIMYFOY 131
 QY 273 IIFVQMPHYDYRNTAIYEQVGLSLHWASLQGLYFLPDWSTRIIMFFLVSHLVGG-- 331
 DB 132 QIIM-----TMVHKNNVDLAWAYS---YYIRFFITYIPFY---GILGALL 171
 QY 331 -----FLLSH---VVTFNHYSVEKFASSNIMSNYACLOQIMTTRNMRPGRFIDWLWGG 380
 DB 172 FLNTRFLESWHFVWVQTNHIVME---IDQAYRDWFSQLTATCNVEQSFENDWFSGH 228
 QY 381 LNYQIEHHLFTPMRHNLTVMPLVKEFAAANGLPY 416
 DB 229 LNFQIEHHLFTPMRHNLTVMPLVKEFAAANGLPY 264

RESULT 15

W84144
 ID W84144 standard; Peptide; 87 AA.
 AC W84144;
 DT 15-FEB-1999 (first entry)
 DE Desaturase enzyme peptide sequence.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846763-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07126.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P,
 PI Thurmond J;
 PI WPI: 98-594582/50.
 DR New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed


```

Db 232 FVEKRLTFDS--LSREFVSQHTFYPIMCAARLNMVQSLIMLLTK-----RNVSY 281
QY 292 -IYEQVGLSLHAWNSLQYFLPDNSTRIMFFLVSHLVGGFLSHVYTFNHYSVKFAFS 350
Db 282 RAQELGCLVFSITWYPLLVSLCPNMGIRIMFVIASLSVTG-MQOVQFSLNHFSVY-VG 339
QY 351 SNMSNACLOQMTTMRMRPGRFDLWGLNGLYQIEHHLFPPTMRNLNTVMPLVKEFAA 410
Db 340 KPGKNWFKEQDGTLDISCPWMDWFGHGLQFQIEHHLFPKPRNLRKISPYTELCK 399
QY 411 ANGLPYMVDYFTGFWELEQFRNIAANAAKTKKI 446
Db 400 KHNLPYNVASFSEKANEMLTLRLNTALQARDITKPL 435

RESULT 12
W84155
ID W84155 standard; Protein: 608 AA.
AC W84155;
DE 15-FEB-1999 (first entry)
KW Human desaturase enzyme encoded by contig 2535.
KW Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome; human;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Homo sapiens.
FH Key
FT Misc_difference 608 /note= "not specified"
PN W09846763-A1.
PD 22-OCT-1998.
PE 10-APR-1998; U07126.
PR 11-APR-1997; US-834655.
PA (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
DR WPI: 98-594582/50.
DR N-PSDB; V63642.
PT New isolated fatty acid desaturase enzymes - used for the production
PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
PT compositions, nutritional compositions, cosmetics or animal feed
PT Example 12; Pages 123-124; 165pp; English.
CC The present sequence is a human desaturase enzyme. The cDNA sequence was
CC identified based on homology between human cDNA sequences and Mortierella
CC alpina desaturase gene sequences. The specification describes methods for
CC desaturating a fatty acid and for producing a desaturated fatty acid by
CC expressing increased levels of a desaturase. The enzyme can be used for
CC desaturating fatty acids. The enzyme can be used to produce
CC polyunsaturated fatty acids, which can be used for treating malnutrition,
CC in pharmaceutical compositions, in cosmetics or in animal feed. The
CC polyunsaturated fatty acids can be used for treating e.g. restenosis
CC after angioplasty, inflammation, rheumatoid arthritis, asthma,
CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
CC can also be used to inhibit platelet aggregation, cause vasodilation,
CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
CC and other side effects caused by non-steroidal anti-inflammatory drugs,
CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
CC encephalomyelitis and chronic fatigue after viral infections, treat
CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
CC inflammatory skin disorders.
CC Sequence 608 AA;

Query Match 12.8%; Score 312.5; DB 1; Length 608;
Best Local Similarity 29.0%; Pred. No. 8.7e-24;
Matches 80; Conservative 46; Mismatches 115; Indels 35; Gaps 6;

QY 153 LPSAILMGVAMQQLGLWILFEHAFHQLFKNRYNDLASFVGNFLQFSSGGKWEKHNVHH 212
| : | : : | | | | : | : : | : | | | | : | : | : | : | : |

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Db 12 LITAFVLATSOAQAGWLQHDYGHLSVYRKPKNHNLVHKFVIGHLKGASANWNNHRHFQHH 71
QY 213 AATNVVGRDGLDLDPFYATVAEHLNNYSQDSVMTFLFRQHVHMTFMLPFLRLSLMLQS 272
Db 72 AKRNFPHKDPDVMNMLHVFVLGEWQPIEYCKKKLKYLPYNNHQHEYFFLIGPLLPIMYFOY 131
QY 273 IIFVSOMPHYDYRYNTAIYEQVGLSHWASLQGLYFLPDWSTRIIMFFLVSHLYGG-- 331
Db 132 QIIM-----TMVHKNMVDLAWVS-----YYIRFFITYPEV---GILGALL 171
QY 331 -----FLLSH-----VVTFNHYSVEKFALSNMSNYACLOIQTMTTRMPRGRIDWMLGG 360
Db 172 FLNFTREFLESHWFVVTQNHIVME---IDQAYRDFWSSQLTATCNVQSQFNDWFSGH 228
QY 381 LNYQIEHHLFPTMPRHLNLTVMPLVKEFAAANGLPY 416
Db 229 LNFQIEHHLFPTMPRHLNLTVMPLVKEFAAANGLPY 264

RESULT 13
W85134
ID W85134 standard; Protein: 608 AA.
AC W85134;
DE 11-FEB-1999 (first entry)
KW A desaturase enzyme encoded by contig 2535.
KW Fatty acid; desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
OS Homo sapiens.
FH Key
FT Misc_difference 608 /note= "not specified"
PN W09846765-A1.
PD 22-OCT-1998.
PE 10-APR-1998; U07422.
PR 11-APR-1997; US-833610.
PA (ABBO ) ABBOTT LAB.
PA (CALJ ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
DR WPI: 99-009334/01.
DR N-PSDB; V82641.
PT New nucleic acid encoding delta5 and other desaturase enzymes -
PT useful in production of oils of increased arachidonic acid content,
PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
PT Claim 87; Pages 117-119; 153pp; English.
CC The present sequence represents a human desaturase enzyme. The enzyme
CC sequence is used in the methods of the invention. The specification
CC describes methods for desaturating a fatty acid and for producing a
CC desaturated fatty acid by expressing increased levels of a desaturase.
CC The enzyme can be used for desaturating fatty acids. The enzyme can be
CC used to produce polyunsaturated fatty acids, which can be used for
CC treating malnutrition, in pharmaceutical compositions, in cosmetics or
CC in animal feed. The polyunsaturated fatty acids can be used for treating
CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
CC They can also be used to inhibit platelet aggregation, cause
CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
CC wall smooth muscle and fibrous tissue, reduce or prevent
CC gastro-intestinal bleeding and other side effects caused by non-steroidal
CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after
CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
CC syndrome, hypertension and inflammatory skin disorders.
CC Sequence 608 AA;

Query Match 12.8%; Score 312.5; DB 1; Length 608;
Best Local Similarity 29.0%; Pred. No. 8.7e-24;
Matches 80; Conservative 46; Mismatches 115; Indels 35; Gaps 6;

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[illegible]

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Query Match      16.8%; Score 409.5; DB 1; Length 448;
Best Local Similarity 27.2%; Pred. No. 5.4e-34;
Matches 124; Conservative 69; Mismatches 198; Indels 65; Gaps 16;

QY 12 FIKDGKWCIDDVAVLSHRPGGS-AITTYKNMDATTVFHTFHTGSKAYOWLTCLKKECP 70
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 24 WISQGRAYDSWDV-KDHPGGSFPLKSLACQEVTDVAFVHPAS-----TW----- 70

QY 71 TOEPEIPDKIDPIKGIDDVNNGFTNFISEKASAINKSFDTLRRVRRAEGLMDG----- 125
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 70 -----KNDLKFTTG-YLKDYSVSEVSKDYRLKLVFEESKMGLYDKKGHMF 114

QY 125 SPLFYIRKILE-TIFTILFAPYLQHTYYLPSAILMGVAAQOOLGWLIEHFAHHQLFNRY 183
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 115 ATLCFIAMLFAMSVVGLFCEGVVHLF--SGCLMGFLWTIQSGWIGHDAGHYVMVSDSR 171

QY 184 YNDIASFVGNFLQFGSSGGHKEQHNVHAATNVVGRGDLDLYP-----FVATVAEH 236
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 172 LNKFMGFIANACLSGISIGWKWNHNAHIACNLSLEXDPDLOYIPFLVSSKFFGSLTSH 231

QY 237 L--NNYSODSVMTLFRHQHWHTF--MLPFLRLSLLQSIFFVSQMPHTHYDYRNTA-- 292
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 232 FYEKRLLTFS--LSRFFVSYQHWTYFPMCAARLNNYVQSILMLTK-----RVVSY 281

QY 292 -IYEOVGLSLHWANSLGQLYLPDWMSTRIMFPLVSLHVGGLLSHWVTFNHYSEVKFALS 350
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 282 RAQELGGLCVSIWYPLLVSLCPNWGERIMFVIASLVTG-MQQVQFSLNHFFSSVY-VG 339

QY 351 SNINMSYACLAQIMTTRNRPGRCFIDWLNGGLNYQTEHLLFPTMPRHNLNTVMPLVKEFAA 410
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 340 KPGKNNWEKQTDGTDLDISCPWMDWFHGGLOFQIEHHLFPKMPRCNLRKISPYIELCK 399

QY 411 ANGLPYWDDVFTGTFWLEIEQFRNTANVAKLTKKI 446
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 400 KHNLPYVAYSFSKANEMTLRTLRNTALQARDITKPL 435

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FT      /label= Metal_box-2
PN      WO9621022-A2.
PD      11-JUL-1996.
PR      28-DEC-1995; IB1167.
PF      30-DEC-1994; US-366779.
PA      (RHON ) RHONE POULENC AGROCHIMIE.
PI      Freysnait GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
DR      WPI; 96-33397/33.
DR      N-PADB: T30395.
PT      Transgenic plants comprising the borage delta-6-desaturase gene
PT      show increased production of gamma linolenic acid and having
PT      increased resistance to chilling
PS      Claim 3; Page 52-53; 75pp; English.
CC      Borage delta-6-desaturase (R98455) catalyses the conversion of
CC      linoleic acid to gamma-linolenic acid (GLA). Its sequence was
CC      deduced from that of the delta-6-desaturase gene (T30395) isolated
CC      from a borage membrane-bound polysomal library. The sequence is
CC      distinct from that of Synecocystis delta-6-desaturase (R98456).
CC      Expression of the desaturase in transgenic plants, esp. sunflower,
CC      soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
CC      increased GLA prodn. Alteration of the plant membrane lipids as a
CC      result of expression of the desaturase may also result in increased
CC      resistance to chilling.
SQ      Sequence 448 AA;

Query Match          16.8%; Score 409.5; DB 1; Length 448;
Best Local Similarity 27.2%; Pred. NO. 5.4e-34;
Matches 124; Conservative 69; Mismatches 198; Indels 65; Gaps 16;

QY 12 FTKDKGKCVIDAVLRSHPGGS-AITTYKNMDATVFHTFTHGSKEAQWLTELKKECP 70
DB   :| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DQ 24 WISIOGKAYDVSDWV-KDHPPGGSEPLKSLAGOEVTDAFVAFHPAS-----TW----- 70
QY 71 TQPEIPDIKDPIRGIDVDNNGTNISKRSAQINKSFETDLRMVRRAEGLMDG----- 125
DB   -:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DQ 70 -----RNLDKFFTG-YLKDYSYSEVSCKYRLKVFEFSKMGLYDKKGHIMF 114
QY 125 SPLFYRKILE-TITILFAFLQVLYHYTLPSAILMGVAWOOLGHLIHEFAHHOLFKNRY 183
DB   -:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DQ 115 ATLCLFIAMLFANSYGVLFCEGVHLF---SGCLMGEFLTOSGWIGHDAGHYMVVSDSR 171
QY 184 YNDLASYFVGNFLOQFGSSGGKKEOHNVHAATNVYGRGDLDLP-----FYATVAEH 236
DB   -:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DQ 172 LNKFMGIFPAAACLSGISIGWNKNHNHAIACNSLEYDPDLOYLPFLVVSKFFGSLTSH 231
QY 237 L--NNYSODSNVMTLFRHQHVHTF--MLPELRSLWLLQSIIFFVSQMPTHYDYIRNTA- 292
DB   -:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DQ 232 FYEKRLFDS--LSRFVSYOHTWFYPIMCAARLNMYQSLIMLTLC-----RVNSY 281
QY 292 -IYEQVGLSLHWANSLGQLYFLPDWSTRIMEFLYSLHVGFLSHVTVFNHYSVEKFALS 350
DB   -:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DQ 282 RAQELGCLVFSIWYPLLVSCLPWNGERIMPVIASLVTC-MQQOVQFSLNHFSVV-VG 339
QY 351 SNMSNVACIQIMTRNMRRPCRFIDLWMGLNGVQIEHLEFPTMPRHNLNTVMPLVKFEAA 410
DB   -:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DQ 340 KPXGNNNFERQTDTGLDISCPPMWDHFHGQLQIEHLEFPKAPCRMLKRISPVIYELCK 399
QY 411 ANGLPYMVDDYFTGFWELEIQEFNRNIANAVALTKKI 446
DB   -:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DQ 400 KHNLPYNASFKANEMTLRTLALQARDITKPL 435

RESULT      9
W67471
ID ID W67471 standard; Protein; 448 AA.
AC AC W67471;
DT 02-WAR-1999 (first entry)
DE Borage delta-6 desaturase protein.
KW Upstream region; regulatory region; sunflower; albumin; seed; expression;
KW lipid metabolism; delta-6 desaturase; transgenic plant.
OS Borago officinalis.
FH Key Location/Qualifiers
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CC containing them are used to produce oils such as linoleic acid, ...
CC arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic acid,
CC stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are
CC used: (i) to treat malnutrition; (ii) in infant feeding formulas, or
CC dietary supplements or substitutes, for use in humans or animals; (iii)
CC for treating disorders associated with inadequate consumption or
CC production of PUFA (or their metabolites such as prostaglandins), e.g.
CC restenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis,
CC psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and
CC (v) as animal feeds. Fragments of the DNA are used as probes to isolate
CC related coding sequences. Recombinant plants can produce high yields of
CC PUFA, since new pathways can be created and unwanted ones suppressed.
CC Plants can be engineered to express oils of particular PUFA composition,
CC e.g. one similar to that in human milk, and product recovery is simpler
CC than with e.g. fish. Sequences W95508-514 represent amino acid sequences
CC of various contigs of human desaturase genes which are similar to the
CC M. alpina desaturase sequences.
SQ Sequence 753 AA;

Query Match 16.9%; Score 412; DB 1; Length 753;
Best Local Similarity 27.0%; Pred. No. 6.4e-34;
Matches 116; Conservative 65; Mismatches 170; Indels 78; Gaps 11;

QY 18 KWCQIDDAV-----LRSHPGGS-AITTYKNMDATTVFHTFHTGSKYAYOMLT-----EL 65
DB 22 RLVVIDKVVNISEFTRHRRGGSVISHYAGODATDFVAFHINKGLVKYMNLSLIGEL 81
QY 66 KKECTOEPIPKDDPIKIGIDVNMGTNISEKSAQINKSFTDLMRVRAGSLMDGS 125
DB 82 SPEQSPFEP-----TKNKELTDEFELRATVERMGLMKAN 116
QY 126 PLFYRKILETI-----FTILFAFYLOYHTYIPLSAILMGVANOQLGWLIEFAHHOLF 179
DB 117 HVFFLLYLLHLLDGAALTLTWVFGTSELPFLCAVLLSAVOQAQAGWLQHDYGHLSVY 176
QY 180 KRYNDLASVYGVNFGSGGGKQBNVHHAATNVVGRDGLDLVPFATVAEHLNN 239
DB 177 RKPKNHLLVHKFVIGHLKGASANNVHRRHFOHAKPNIFHKDPDVMNMLHVFVLSGEWQPIE 236
QY 240 YSODSWMTLFRWQHVTMFLPFLRLSLWLSQIFVSQMPHTYDYRYNRTAIYEQVGLS 299
DB 237 YGKKKLYLPYNHCHQHEVFFLIGPPLIPMYFOYQIIM-----TMIHKNWVD 283
QY 300 LHWANSLGOLYFLPDWSTRMFFLVSHLVGG-----FLLSH-----VVFNFHYSVEKF 347
DB 284 LAWAVS-----YYIRFFITYIPFY---GILGALLFLNFRFLESHWFWVWVTONNHVME-- 335
QY 348 ALSSNINSYACLOIMTTRNMGRFRIDWLWGLNYQIEHHLFTMPRHNLTNVMPLVKE 407
DB 335 -IDQAYRDWFSSQLTATCNVEQSFNDWFSGHLNFQIEHHLFTMPRHNLTNVMPLVKS 393
QY 408 FAANGLPY 416
DB 394 LCAKHGIEY 402

RESULT 8
R98455
ID R98455 standard; Protein; 448 AA.
AC R98455;
DT 15-SEP-1996 (first entry)
DE Borage delta-6-desaturase.
KW Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
KW polyunsaturated fatty acid; octadecatetraenoic acid;
KW chilling resistance; oilseed.
OS Borage officinalis.
FH Key location/Qualifiers
FT 156..163
FT /label= Lipid_box
FT 196..200
FT /label= Metal_box-1
FT 372..377

DB 177 RKPKNHLLVHKFVIGHLKGASANNVHRRHFOHAKPNIFHKDPDVMNMLHVFVLSGEWQPIE 236
QY 240 YSODSWMTLFRWQHVTMFLPFLRLSLWLSQIFVSQMPHTYDYRYNRTAIYEQVGLS 299
DB 237 YGKKKLYLPYNHCHQHEVFFLIGPPLIPMYFOYQIIM-----TMIHKNWVD 283
QY 300 LHWANSLGOLYFLPDWSTRMFFLVSHLVGG-----FLLSH-----VVFNFHYSVEKF 347
DB 284 LAWAVS-----YYIRFFITYIPFY---GILGALLFLNFRFLESHWFWVWVTONNHVME-- 335
QY 348 ALSSNINSYACLOIMTTRNMGRFRIDWLWGLNYQIEHHLFTMPRHNLTNVMPLVKE 407
DB 335 -IDQAYRDWFSSQLTATCNVEQSFNDWFSGHLNFQIEHHLFTMPRHNLTNVMPLVKS 393
QY 408 FAANGLPY 416
DB 394 LCAKHGIEY 402

RESULT 7
W95514
ID W95514 standard; Protein; 753 AA.
AC W95514;
DT 26-MAR-1999 (first entry)
DE Amino acid sequence of human desaturase gene contig 253538a.
KW Delta 5 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil;
KW polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic;
KW stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula;
KW dietary supplement; prostaglandin; restenosis; angioplasty; inflammation;
KW rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS;
KW diabetes; cosmetic; animal feed; human.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 433 /note= "encoded by TGA"
FT Misc_difference 459 /note= "encoded by TGA"
FT Misc_difference 596 /note= "encoded by TGA"
FT Misc_difference 629 /note= "encoded by TGA"
FT Misc_difference 655 /note= "encoded by TAG"
FT Misc_difference 673 /note= "encoded by TGA"
FT Misc_difference 688 /note= "encoded by TGA"
FT Misc_difference 753 /note= "encoded by TG"
PN W09846764-A1.
PD 22-OCT-1998.
PF 10-APR-1998; U07421.
PR 24-OCT-1997; US-956985.
PR 11-APR-1997; US-833610.
PR 11-APR-1997; US-834033.
PR 11-APR-1997; US-834655.
PA (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
PI Thurmond J;
DR N-PSDB; X00910.
DR WPI; 99-080739/07.
PT Nucleic acid construct able to express fatty acid desaturase in
PT plants - useful in human or animal nutrition, as cosmetics and
PT therapeutically, e.g. for restenosis, cancer and diabetes
PS Claim 48; page 169-171; 210pp; English.
CC The invention relates to a nucleic acid construct that contains at least
CC one of the nucleotide sequences (X00889 to X00891) encoding Mortierella
CC alpina delta 6, delta 12 and delta 5 desaturases (W95504 to W95506)
CC respectively, coupled to an expression control sequence functional in
CC plants. Recombinant plant cells containing at least one DNA encoding a
CC M. alpina fatty acid desaturase (FAD), can be used for the production of
CC polyunsaturated fatty acid (PUFA). These recombinant cells or plants

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 746 /note= "not specified"
 PN WO9846763-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07126.
 PR 11-APR-1997; US-834655.
 PA (ABBO) ABBOTT LAB.
 PI (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmmond J;
 DR WP: 98-594582/50.
 DR N-PSDB: V63643.
 PR New isolated fatty acid desaturase enzymes - used for the production
 PT of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed
 PS Example 12: Pages 124-126; 155pp; English.
 CC The present sequence is a human desaturase enzyme. The cDNA sequence was
 CC identified based on homology between human cDNA sequences and Mortierella
 CC alpina desaturase gene sequences. The specification describes methods for
 CC desaturating a fatty acid and for producing a desaturated fatty acid by
 CC expressing increased levels of a desaturase. The enzyme can be used for
 CC desaturating fatty acids. The enzyme can be used to produce
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma,
 CC psoriasis, cancer, diabetes or eczema or reduce blood pressure. They
 CC can also be used to inhibit platelet aggregation, cause vasodilation,
 CC lower cholesterol levels, inhibit proliferation of vessel wall smooth
 CC muscle and fibrous tissue, reduce or prevent gastro-intestinal bleeding
 CC and other side effects caused by non-steroidal anti-inflammatory drugs,
 CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
 CC encephalomyelitis and chronic fatigue after viral infections, treat
 CC AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and
 CC inflammatory skin disorders.
 SQ Sequence 746 AA;

Query Match 16.9%; Score 412; DB 1; Length 746;
 Best Local Similarity 27.0%; Pred. No. 6.3e-34;
 Matches 116; Conservative 65; Mismatches 170; Indels 78; Gaps 11;

QY 18 KWCQIDDAV-----LRSHPGGS-AITTKNDATTFTHTGSKAEYQWLT-----EL 65
 DB 22 RNLVIDRKVYNISEFTRRHPPGGSRVISHYAGODATDPFVAFHINKGLVKYKNSLLIGEL 81
 QY 66 KKECTQPEIPDKDDPIKIGIDVNMGTNFNISEKRSQAQINKSFDTLDRMRVRAEGLMDGS 125
 DB 82 SPEQPSFEP-----TKNKELTDEFRELATRVEMGLMKAN 116
 QY 126 PLFYIRKILETI-----FTILFAFYLYQHTYTPSAILMGVAMQGLWLIHEFAHOLF 179
 DB 117 HVFFLLVLLHLLDGAANLTLWVFGTSFLPFLCAVLLSAVQQAQAGWLQHDYGHLSVY 176
 QY 180 KNYRYNDLASVFNQFLOGSSGKWEQHNVHHAATNVYRGDGLDLPVPFYATVAEHLNN 239
 DB 177 RPKWNHLVHKFVICHKLKASANNHRRHQHAKPNIFHKDPDYNMLRVFVLGEWQPIE 236
 QY 240 YSDSWYMTLFRWQHVTWFMPLFRLSLWLLQSIFVSQMTHTYDYIRNTAIVEQVGLS 299
 DB 237 YGKKKLYLPNHQHEFFLLGPPLLIPMYFYQIIM-----TMIVHKNVVD 283
 QY 300 LHWAMSGQLYFLPDWSTRMIFLVSLVGG-----FLLSH-----VYTFNHYSEKFP 347
 DB 284 LAWAVS-----YYIRFFITYPFY---GILGALLFELNIRFLESWFVWVTOMNHVME-- 335
 QY 348 ALSNMSNTACIQWITRNMRPGRFIDWLWGLNLYQIEHFLFTMPRHNLNTVPLVKE 407
 DB 335 -IDQAYRDWFSSQLTATCNVEQSFENDWFSGLHNFQIEHFLFTMPRHNLHKLAPLVKS 393
 QY 408 FAANGLPY 416

DB 394 LCAKHGIEY 402

RESULT 6

W85135
 ID W85135 standard; Protein; 746 AA.
 AC W85135;
 DT 11-FEB-1999 (first entry)
 DE A desaturase enzyme encoded by contig 253538a.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 746 /note= "not specified"
 PN WO9846765-A1.
 PD 22-OCT-1998.
 PF 10-APR-1998; U07422.
 PR 11-APR-1997; US-833610.
 PA (ABBO) ABBOTT LAB.
 PI (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmmond J;
 DR WP: 99-009334/01.
 DR N-PSDB: V83642.
 PR New nucleic acid encoding delta5 and other desaturase enzymes -
 PT useful in production of oils of increased arachidonic acid content,
 PT used, e.g. for treating cancer, as foods, animal feeds and cosmetics
 PS Claim 87; Pages 119-120; 153pp; English.
 CC The present sequence represents a human desaturase enzyme. The enzyme
 CC sequence is used in the methods of the invention. The specification
 CC describes methods for desaturating a fatty acid and for producing a
 CC desaturated fatty acid by expressing increased levels of a desaturase.
 CC The enzyme can be used for desaturating fatty acids. The enzyme can be
 CC used to produce polyunsaturated fatty acids, which can be used for
 CC treating malnutrition, in pharmaceutical compositions, in cosmetics or
 CC in animal feed. The polyunsaturated fatty acids can be used for treating
 CC e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis,
 CC asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure.
 CC They can also be used to inhibit platelet aggregation, cause
 CC vasodilation, lower cholesterol levels, inhibit proliferation of vessel
 CC wall smooth muscle and fibrous tissue, reduce or prevent
 CC gastro-intestinal bleeding and other side effects caused by non-steroidal
 CC anti-inflammatory drugs, prevent or treat endometriosis and premenstrual
 CC syndrome, treat myalgic encephalomyelitis and chronic fatigue after
 CC viral infections, treat AIDS, multiple sclerosis, acute respiratory
 CC syndrome, hypertension and inflammatory skin disorders.
 SQ Sequence 746 AA;

Query Match 16.9%; Score 412; DB 1; Length 746;
 Best Local Similarity 27.0%; Pred. No. 6.3e-34;
 Matches 116; Conservative 65; Mismatches 170; Indels 78; Gaps 11;

QY 18 KWCQIDDAV-----LRSHPGGS-AITTKNDATTFTHTGSKAEYQWLT-----EL 65
 DB 22 RNLVIDRKVYNISEFTRRHPPGGSRVISHYAGODATDPFVAFHINKGLVKYKNSLLIGEL 81
 QY 66 KKECTQPEIPDKDDPIKIGIDVNMGTNFNISEKRSQAQINKSFDTLDRMRVRAEGLMDGS 125
 DB 82 SPEQPSFEP-----TKNKELTDEFRELATRVEMGLMKAN 116
 QY 126 PLFYIRKILETI-----FTILFAFYLYQHTYTPSAILMGVAMQGLWLIHEFAHOLF 179
 DB 117 HVFFLLVLLHLLDGAANLTLWVFGTSFLPFLCAVLLSAVQQAQAGWLQHDYGHLSVY 176
 QY 180 KNYRYNDLASVFNQFLOGSSGKWEQHNVHHAATNVYRGDGLDLPVPFYATVAEHLNN 239

CC for producing a desaturated fatty acid by expressing increased levels of
 CC a desaturase. The present desaturase is an enzyme which introduces a
 CC double bond carbons 6 and 7 from the carboxyl end of a fatty acid
 CC molecule. The enzyme can be used for desaturating fatty acids. The
 CC enzyme can be used to produce polyunsaturated fatty acids, which can
 CC be used for treating malnutrition, in pharmaceutical compositions,
 CC in cosmetics or in animal feed. The polyunsaturated fatty acids can
 CC be used for treating e.g. restenosis after angioplasty, inflammation,
 CC rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema
 CC or reduce blood pressure. They can also be used to inhibit platelet
 CC aggregation, cause vasodilation, lower cholesterol levels, inhibit
 CC proliferation of vessel wall smooth muscle and fibrous tissue,
 CC reduce or prevent gastro-intestinal bleeding and other side effects
 CC caused by non-steroidal anti-inflammatory drugs, prevent or treat
 CC endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
 CC and chronic fatigue after viral infections, treat AIDS, multiple
 CC sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
 CC disorders.
 SQ Sequence 457 AA;

Query Match 25.5%; Score 620; DB 1; Length 457;
 Best Local Similarity 32.8%; Pred. No. 1e-55;
 Matches 153; Conservative 76; Mismatches 176; Indels 62; Gaps 13;

QY 4 REQHEPFKIDKWCQIDAVLRSHPGSGSAITTYKNNDAITVPHFTGSKAYQWLT 63
 DB 25 KKDAEAPFLMIDNKVDYREFV-PDHGSGVILTHVGKDGTDVETPH---PEA-AWET 79
 QY 64 ELKKECPQPEIPDKDDPIKGDIDVNGTGNISEKSAQINKSFDTLRMRVRAEGLMD 123
 DB 80 LANFVVGDIIDSDRDIKNDF-----AAEVRK-----LRTLFQSLGYD 118
 QY 124 GSPFYIRKI-----LETIFTLFAFYLOYHTY-YLPSAILMGVAQOGLWLIHEFAHQ 177
 DB 119 SSKAYAFKVSFNLGSLGSLVIVAKWGOTSTLANVLSAALGLFVQCGWLAHDFLHQ 178
 QY 178 LFNRYNDLASYFYVGNFQSGGKQHNHVAATNVYGRDGLDLPFYATVAEHL 237
 DB 179 VFQDFWGLDLCFALGGVCGFSSSWKDKHNTHAAPNVHVEDPDIDTHPL-LTWEHA 237
 QY 238 NNYSD-----SWMTLFRQHVHTF--MLPFLRLSWLLSIIIV-----SQ 278
 DB 238 LEMFSDVPDEELTRMWSRFLVNTWTFYFPLSLFARLSWCLQSILFVLPNGQAKPSGAR 297
 QY 279 MPTHYDYRYNTAIYEQVGLSLHWAWSLGQLY-FLPDWSTRIIMFVLVSHVGGLSHVY 337
 DB 298 VP-----ISLVEQLSLAMHHTWYLTATMFLFKDPVNMVLYFLVSOAVCGNLLAIVF 348
 QY 338 TFNHYSVEKFASSNIMSYACLOIMTRMRPGRFIDMLWGGLNYQIEHHLFPTMPRH 397
 DB 349 SLNHGMPVISKEEAVDMDFTKQITGRDVHPGLFANFTGGLNYQIEHHLFPTMPRH 408
 QY 398 LNTVMPLVKEFAAANGPLVMDYFTGFWLEIEQFRNIANYAAKLTK 444
 DB 409 FSKIQPAVETLCKKYNVRYHTTGMEICTAEVFSRLNEVSKAASKMGK 455

RESULT 4
 W84139
 ID W84139 standard; Peptide: 355 AA.
 AC W84139;
 DT 15-FEB-1999 (first entry)
 DE Desaturase enzyme peptide sequence.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.
 OS Unidentified.
 PN W09846763-A1.
 PD 22-OCT-1998.

FF 10-APR-1998; U07126.
 PR 11-APR-1997; US-834655.
 PA (ARBO) ABBOTT LAB.
 PA (CALJ) CALGENE LLC.
 PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P,
 PI Thurmond J;
 DR WPI; 98-594582/50.

DR New isolated fatty acid desaturase enzymes - used for the production
 of polyunsaturated fatty acids for use in, e.g. pharmaceutical
 PT compositions, nutritional compositions, cosmetics or animal feed
 PT Example 2; Pages 101-102; 165pp; English.
 PS The present sequence represents a peptide derived from a desaturase
 CC enzyme. The specification describes methods for desaturating a
 CC fatty acid and for producing a desaturated fatty acid by expressing
 CC increased levels of a desaturase. Desaturases can be used for
 CC desaturating fatty acids. The enzymes can be used to produce
 CC polyunsaturated fatty acids, which can be used for treating malnutrition,
 CC in pharmaceutical compositions, in cosmetics or in animal feed. The
 CC polyunsaturated fatty acids can be used for treating e.g. restenosis
 CC after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis,
 CC cancer, diabetes or eczema or reduce blood pressure. They can also be
 CC used to inhibit platelet aggregation, cause vasodilation, lower
 CC cholesterol levels, inhibit proliferation of vessel wall smooth muscle
 CC and fibrous tissue, reduce or prevent gastro-intestinal bleeding and
 CC other side effects caused by non-steroidal anti-inflammatory drugs,
 CC prevent or treat endometriosis and premenstrual syndrome, treat myalgic
 CC encephalomyelitis and chronic fatigue after viral infections, treat AIDS,
 CC multiple sclerosis, acute respiratory syndrome, hypertension and
 CC inflammatory skin disorders.
 SQ Sequence 355 AA;

Query Match 22.8%; Score 555; DB 1; Length 355;
 Best Local Similarity 34.5%; Pred. No. 3.6e-49;
 Matches 124; Conservative 65; Mismatches 134; Indels 36; Gaps 8;

QY 112 LMRVRAEGLMDGSPFYIRKI-----LETIFTLFAFYLOYHTY-YLPSAILMGVAQO 165
 DB 5 LRTLFQSLGYDSSKAYAFKVSFNLGSLVIVAKWGOTSTLANVLSAALGLFVQO 64
 QY 166 LGWLHFEFAHOLFKNRYNDLASYFYVGNFQSGGKQHNHVAATNVYGRDGLD 225
 DB 65 CGWLHADFHLHQVDFQDFWGLDLCFALGGVCGFSSSWKDKHNTHAAPNVHGEDPDID 124
 QY 226 LVPFYATVAEHLNNSQD-----SWMTLFRQHVHTF--MLPFLRLSWLLSIIIV- 277
 DB 125 THPL-LTWEHALEMFSDVPDEELTRMWSRFLVNTWTFYFPLSLFARLSWCLQSILFVL 183
 QY 277 -----SQMPTHYDYRYNTAIYEQVGLSLHWAWSLGQLY-FLPDWSTRIIMFVLV 325
 DB 184 PNGQAKPSGARVP-----ISLVEQLSLAMHHTWYLTATMFLFKDPVNMVLYFLV 234
 QY 326 HLVGGLLSHVYTFNHYSVKEKFASSNIMSYACLOIMTRMRPGRFIDMLWGGLNYOI 385
 DB 235 QAVCGNLLAIVFLSNHGMPIVSKKEEAVDMDFTKQITGRDVHPGLFANFTGGLNYOI 294
 QY 386 EHLFPTMPRHNLNTVMPLVKEFAAANGPLVMDYFTGFWLEIEQFRNIANYAAKLTK 444
 DB 295 EHLFPTMPRHNFPSKIQPAVETLCKKYNVRYHTTGMEICTAEVFSRLNEVSKAASKMGK 353

RESULT 5
 W84156
 ID W84156 standard; Protein: 746 AA.
 AC W84156;
 DT 15-FEB-1999 (first entry)
 DE Human desaturase enzyme encoded by contig 253538a.
 KW Fatty acid; desaturase; polyunsaturated fatty acid;
 KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
 KW cholesterol level; endometriosis; premenstrual syndrome; human;
 KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
 KW acute respiratory syndrome; hypertension; inflammatory skin disorder.

Db 134 LGHVEIHGDGAVRMSPEOEHVG-----IYRFQFIWGLYL-FIPFWFLYDYI 182
 Qy 275 FYSQMPHYDY-----YRNTAYEOVGLSLHWMSGLQYFLPDWSTRMFFLVSHLVGG 330
 Db 183 LVLN-KGKYHDKIPPFPQLEASLIGIKLLW---LGYVGLP---LALGFSIPEVLIGA 235
 Qy 331 -----FLSHVVTNFNHYSVKFASSNMSNACLOIMTTRNMRPGR-FID 375
 Db 236 SVTYMTGIWCTIFMLAHVLESTF-LTPDGESGAIDDEWAICQITANFATNPFWN 294
 Qy 376 WLGGLNLYQIEHLFTPMRHNLTNMPVLYKEFAAANGLPYVDDYFTGF-----WLE 428
 Db 295 WFCGGLNHQVTHLFPFNICHYPOLENIKQVCEGVEYKVPYPTFKAAIASNYRWLE 353

RESULT 2
 ID FD61_SOYBN STANDARD; PRT: 387 AA.
 AC P48630;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 1
 DE (EC 1.14.99.-)
 GN FAD2-1.
 OS Glycine (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
 OC Glycine.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED.
 RX MEDLINE; 96151506.
 RA HEPPARD E.P., KINNEY A.J., STECCA K.L., MIAO G.H.;
 RT "Developmental and growth temperature regulation of two different
 RT microsomal omega-6 desaturase genes in soybeans.";
 RL Plant Physiol. 110:311-319(1996).
 CC -|- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -|- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -|- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.
 CC -|- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -|- SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.
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 CC -----
 CC EMBL; LA3920; AAB00859.1;
 DR PFAM; PF00487; FA_desaturase; 2.
 KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KW Transmembrane.
 FT TRANSMEM 54 74 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 FT TRANSMEM 121 141 POTENTIAL.
 FT TRANSMEM 183 203 POTENTIAL.
 FT TRANSMEM 227 247 POTENTIAL.
 FT ANSHEM 251 271 POTENTIAL.
 FT MAIN 109 113 HISTIDINE BOX 1.
 FT MAIN 145 149 HISTIDINE BOX 2.
 FT MAIN 319 323 HISTIDINE BOX 3.

SQ SEQUENCE 387 AA; 44662 MW; 9F81BE96 CRC32;

Query Match 6.8%; Score 165.5; DB 1; Length 31
 Best Local Similarity 23.3%; Pred. No. 1.7e-05;
 Matches 88; Conservative 44; Mismatches 115; Indels 1

Qy 126 PLFYRKILET---ILETLEAFYLOQYHTY---LP---SAILMGVAVOOLG--
 Db 47 PICFQSLTSSYVYDLSFAFIYFIATYTHLLPQPSLAWPIYVWLOGCLL

Qy 170 I-HEFAHHOLFKNRYND-----LASVYVGNFLOGFSSGGWKEQHNHHAATNVV 218
 Db 107 IAHECGHAFSKYQWDDVGLTSLTLLVPYF-----SNKISHRRHHSNTGSL 155

Qy 219 GRDGDLDLVP--FYATVAEHLNNYSQDSWNTLFRHQHWHWTMLPFLRLSLWLOSIFV 276
 Db 156 DRDEVEVPKPKSVAMFSLYNN-----PLGR-----AVSLVTLTIGWPMYLAFN 202

Qy 277 SQMP-----THYDY---YRN-----TAIYBOVGLSLHWMSL-GOLYFLPDWST 317
 Db 203 SGRPYDSFASHYHPYAPIYSNRERLLIYSDVALF-SVYSLYRVATLKGVLWLLCYGV 261

Qy 318 RIMFFFLVSHLVGGFLLSHVVTNFNHYSVKFASSNMSNACLOIMTTRNMRPGRFIDWL 377
 Db 262 PLL-----IVNGFL---VTITLQHTHALPHYDSEW-----DWL 294

Qy 378 WGLG-----NYQIEHLFTPMRHN-----LNTVMPLVKEFAAANGLP 415
 Db 295 KGAATMDRDYGLNKVFHHITDTHVAHLLFTMPHYHAMEATNAIKPILGEY----- 348

Qy 416 YVDD--YFTGFWLEIEO 431

Db 348 YQFDDTFFYKALWREARE 365

RESULT 3

ID FD6E_ARATH

AC P46313; STANDARD; PRT: 383 AA.

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)

DE (DELTA-12 DESATURASE).

GN FAD2.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;

OC Arabidopsis.

CC [1]

CC SEQUENCE FROM N.A.

CC MEDLINE; 94176997.

CC OKULEY J., LIGHTNER J., FELDMANN K.A., YADAV N., LARK E., BROWSE J.;

CC "Arabidopsis FAD2 gene encodes the enzyme that is essential for

CC polyunsaturated lipid synthesis.";

CC Plant Cell 6:147-158(1994).

CC -|- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES

CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.

CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE

CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS

CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER

CC PHOSPHOLIPIDS.

CC -|- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.

CC -|- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.

CC -|- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE

CC AND/ OR BE INVOLVED IN METAL ION BINDING.

CC -|- SIMILARITY: TO OTHER PLANT ER OMEGA-6 FATTY ACID DESATURASES.

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[1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 92032774.
RA SMART L.B., MCINTOSH L.:
RT "Expression of photosynthesis genes in the cyanobacterium
RT Synechocystis sp. PCC 6803: psaa-psab and psba transcripts accumulate
RT in dark-grown cells.";
RL Plant Mol. Biol. 17:959-971(1991).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE: 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA OKUSUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,
RA OKUMURA S., SHIMO S., TAKEUCHI C., WADA T., WATANABE A.,
RA YAMADA M., YASUDA M., TABATA S.:
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- FUNCTION: PSAA ALONG WITH PSAB BIND P700, THE PRIMARY ELECTRON
CC DONOR OF PHOTOSYSTEM I (PSI) AS WELL AS THE ELECTRON ACCEPTORS A0,
CC A1, AND FX.
CC -!- COFACTOR: P700 IS A CHLOROPHYL DIMER, A0 IS CHLOROPHYLL, A1 IS A
CC PHYLLOQUINONE AND FX IS A 4FE-4S IRON-SULFUR CENTER.
CC -!- SUBUNIT: HETERODIMER OF A1 AND A2 SUBUNITS WHICH BIND TOGETHER THE
CC IRON-SULFUR CENTER FX.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE PSAA/PSAB FAMILY.
CC -----
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CC -----
DR EMBL: X58825; CA441630.1; -;
DR EMBL: D90906; BA417438.1; -;
DR PIR: S18243; S18243.
DR PIR: S19090; S19090.
DR PROSITE: PS00419; PHOTOSYSTEM_I_PSAAB; 1.
DR PFAM: PF00223; psaa_psab; 1.
KW Chlorophyll; Photosystem I; Electron transport; Photosynthesis;
KW Transmembrane; Iron-sulfur; 4Fe-4S.
FT INIT_MET 0 BY SIMILARITY.
FT TRANSMEM 45 68 I (POTENTIAL).
FT TRANSMEM 134 156 II (POTENTIAL).
FT TRANSMEM 174 198 III (POTENTIAL).
FT TRANSMEM 272 290 IV (POTENTIAL).
FT TRANSMEM 327 350 V (POTENTIAL).
FT TRANSMEM 366 392 VI (POTENTIAL).
FT TRANSMEM 414 436 VII (POTENTIAL).
FT TRANSMEM 513 531 VIII (POTENTIAL).
FT TRANSMEM 571 592 IX (POTENTIAL).
FT TRANSMEM 639 661 X (POTENTIAL).
FT TRANSMEM 703 723 XI (POTENTIAL).
FT TRANSMEM 555 555 IRON-SULFUR (4FE-4S).
FT METAL 564 564 IRON-SULFUR (4FE-4S).
FT METAL 536 537 DA -> ES (IN REF. 1).
SQ SEQUENCE 730 AA; 81160 MW; 7387ELAA CRC32;

Query Match 4.1%; Score 101; DB 1; Length 730;
Best Local Similarity 22.5%; Pred. No. 2.4;
Matches 89; Conservative 48; Mismatches 132; Indels 126; Gaps 24;

OY 26 VLRSHPGGAITYKNMDATVFTHTGSKAYQWLTCLKKCPQEPIDKDDPK 85
DB 45 IFASHFGHIAIFL-WTSGTLFHVAVQGNFE--QWIKD-----PLNIRPIAHAIWDPHF 95
OY 86 GIDVNMGTFTNISKRSAINKSFTDLRMVRAEGLMDGSPLF--YIRKILETITILF 142

Db	96	GEQAVNAFT---QAGASNPVNIAYSGVYHWFYITGMTTNGELYSQAVFLLVLSLF--LF	150
OY	143	AFYLOXYHTYPLPSAILMGVAVQOOLGWLIIHEFAHQLEKN---RYNDLASFEYVGNFLQGE	199
Db	151	AGWLHLQPKFRPS-----LAW-----FKNAESRLNHHLAGLF-----GV	184
OY	200	SSGGWKQEHNVVHAATNV-----VGRDGLD-----LVPEYA-----TVAEHLN	238
Db	185	SSLAW-AGHLVHVAIPEARGCHVGDWDFLSTPPHPAGLMPFFTCGNWGVYAADPDAGHIF	243
OY	239	NYSDS-----WVMTLFRQHVHWTMLPFL-----RLSN-----LL	270
Db	244	GTSEGACTAILTFLGGFHPQTESLWLTDI---AHHLIAIVIFIAGHYMTNNGIGHSI	300
OY	271	OSIFVQSMP-----THYYDYRNTAIYEQVGLSLHWMSLG-----QLYFLP---	314
Db	301	KEILNAHKGPLTGAGHTNLYDTI--NNSLHFQLGLALA---SLGVITSLVAQHMYSLPSYA	356
OY	314	----DMSIRIMFFLVSHLVGGLLSHVVTNNHYSV	344
Db	357	FIAQDHTTAAALYTHHQYIAGFLM--VGAFAGHAI	389

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Job time: 16500 sec

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CC EMBL; AL021287; CAAL6128.1; -;
CC DR PROSITE; PS00077; COX1; 1;
CC DR PFAM; PF00115; COX1; 1;
CC KW Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain.
CC FT TRANSMEM 40 60
CC FT TRANSMEM 89 109
CC FT TRANSMEM 121 141
CC FT TRANSMEM 170 190
CC FT TRANSMEM 213 233
CC FT TRANSMEM 258 278
CC FT TRANSMEM 290 310
CC FT TRANSMEM 315 335
CC FT TRANSMEM 359 379
CC FT TRANSMEM 398 418
CC FT TRANSMEM 433 453
CC FT TRANSMEM 476 496
CC FT METAL 86 86
CC FT METAL 264 284
CC FT METAL 268 288
CC FT METAL 313 313
CC FT METAL 314 314
CC FT METAL 397 397
CC FT METAL 399 399
CC SQ SEQUENCE 573 AA; 63672 MW; 79CD8326 CRC32;

Query Match 4.2%; Score 102.5; DB 1; Length 573;
Best Local Similarity 21.8%; Pred. No. 1.4;
Matches 89; Conservative 49; Mismatches 115; Indels 155; Gaps 25;

QY 116 VRAEGL-MDGSPLFYIRKILETITLAFYQYHTYVLPSSAILMGVA----- 163
DB 196 MRAPGTMERMPF-TWNIWVTSILIAFPLL-----TAALFGLAADRHLGAHYDA 247

QY 163 -----WQQLGWLHIEFAHQLF-----KNNRYNDLASVYGVNQLQ 197
DB 248 ANGVLMLWHLWF---FGHPEYIIALPFGIVSEIFVFSRKPFGYTLTVATLSIA 304

QY 198 GFSSGGWKEQHNVHHA-ATNVVGRDGLDLVPFYA-----TVAEHLNYSQDSWVM 247
DB 305 ALSAVM-----AHMFATGAV-----LLPEFSFTYLIATVGTGKFFN-----WIG 346

QY 248 TLFERWQHVHT-----FMLPELRLSWLLQSIIFVSQMPHYDYIRNTAIYEQV----- 297
DB 347 TMKKGQLTFETPMLFSVGVNVTFL-LGLATGVLLASPLDFHVTDSYFVAHFHYVLPFGT 405

QY 297 -----GLSLHNAW-----SLGQLYFLPDNSTRIMF---FLVSHLVG----- 330
DB 406 IVFATFAGI---YFWFPMKTRGLDERLGLHF---WLTFTGFTTFLVQHWLGDGMPR 459

QY 330 -----GFLLSHVVTENHYSVEKALSS-----NIMSNVACIQIMTRNMRPGR 373
DB 460 RYADLPDQFQGLNVVS-----TIGAFILGASMEPFWNVKFSWRYGEVVI----- 507

QY 374 IDMLGGLNTQIEHHLFPTPRHNLNTVPLVKFEFAAANGL---PYMYD 419
DB 507 VDPWGYGN-SLEWATSCPPPRHNF-TELPRISERPAFELHYPHMVE 552

RESULT 15
PSAB_SYNY3
ID PSAB_SYNY3 STANDARD; PRT; 730 AA.

AC P29255; P73398;
DT 01-DEC-1992 (Rel. 24, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2.
GN PSAB OR SLR1835.

OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

Query Match 4.4%; Score 106; DB 1; Length 424;
Best Local Similarity 21.6%; Pred. No. 0.55;
Matches 59; Conservative 43; Mismatches 115; Indels 56; Gaps 11;

QY 158 LMGVAWQQLGLI-----HEFAHQLFKNRYNDLASVYGVNLF---QGFSSGGWKEQ 207
DB 145 LLPLAVWVTGTAITGFFVIGHDCAHRSFSSNKLVEDI-----VGTAFMPLIYIYEPWRFK 200

QY 208 HNVHHAATNVVGRD-----GDLVPPYATVAEHLNYSQDSWMTLFRWQHVHTF 259
DB 201 HNRHAKTNMLREDTAWHPWKDEFPSTPLLRKAI---IYCYGPFRCWMSIAHW---LWVHF 256

QY 260 MLPELRLSWLLQSIIFVSQMPHYDYIRNTAIYEQVGLSLHNAWSLQGL-YELPDWSTR 318
DB 257 DLKKFR-----PSEVP-----RVKISLACVFAFIAIGWPLLIYKTG 292

QY 319 IM-----FFLVSHLVGFLSHVVTFNHYSVEKALSSNIMSNVACIQIMTRNMRPGRFI 374
DB 293 IMGWIKFWLMPWLYGFHWS-TFTMVHTTAPYIPFYISEWNRAQAQLNGTVHCDYPKWI 351

QY 375 DMLWGLNLYQIEHHLFPTPRHNLNTVMPLVKE 407
DB 352 EILCHDINVHIPHISPRIPSYNLRAHKSQZE 384

RESULT 14
COX1_MYCTU
ID COX1_MYCTU STANDARD; PRT; 573 AA.

AC O53290;
DT 15-DEC-1999 (Rel. 39, Created)

DT 15-DEC-1999 (Rel. 39, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)

DE PROBABLE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (CYTOCHROME
DE AA3 SUBUNIT 1).

GN CTAD OR RV3043C OR MTV012.58C.
OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-H37RV;
RX MEDLINE; 98295987.

RA COLE S.T., BROSCHE R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,
RA GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F.,

RA BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
RA DAVIES R., DEVLIN K., FELTWEILL T., GENTLES S., HAMLIN N., HOLROYD S.,

RA HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MORPHY L.,
RA OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.,

RA RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQUARES R., SULSTON J.E.,
RA TAYLOR K., WHITEHEAD S., BARRELL B.G.;

RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."

RL Nature 393:537-544 (1998).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE

CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +
CC 4 FERROCYTOCHROME C.

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC -----

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QY 356 -NYA-CLOIMTRMRPGRIDMLWGLNLTQIEHHLLPPTMTRNLTNTVMTPLVKEFAAANG 413
 DB 484 LTAECFLMDRRGTIP--FFTTHRSVDF-----FNTDAEKI-TQLPWRAYALSSG 534
 QY 414 LPYVDDYFTGFWL-----EIEOPRNIAVAAKLTK 444
 DB 535 ASIEGPGFTGGNLLFLKSSNSIAKFKVTLNSAALLQR 573

RESULT 12
 YAL7 SYN3
 ID YAL7 SYN3 STANDARD; PRT; 442 AA.
 AC P72935;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE PUTATIVE AMMONIUM TRANSPORTER SLL1017.
 GN SLL1017
 OS Synecocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,
 RA OKUMURA S., SHIMO S., TAKEUCHI C., WADA T., WATANABE A.,
 RA YAMADA M., YASUDA M., TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synecocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
 CC -!- SIMILARITY: BELONGS TO THE AMT1/MEP/NRGA FAMILY OF AMMONIUM
 CC TRANSPORTERS (TC 2.49).
 CC
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 CC
 CC EMBL; D90901; BAAL6952.1;
 DR PROSITE; PS01219; AMMONIUM_TRANS; 1.
 DR PFAM; PF00909; Ammonium_transp; 1.
 KW Hypothetical protein; Transp; Transmembrane.
 FT TRANSMEM 5 25 POTENTIAL.
 FT TRANSMEM 44 64 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 104 124 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.
 FT TRANSMEM 155 175 POTENTIAL.
 FT TRANSMEM 193 213 POTENTIAL.
 FT TRANSMEM 240 260 POTENTIAL.
 FT TRANSMEM 269 289 POTENTIAL.
 FT TRANSMEM 299 319 POTENTIAL.
 FT TRANSMEM 325 345 POTENTIAL.
 FT TRANSMEM 354 374 POTENTIAL.
 FT TRANSMEM 386 406 POTENTIAL.
 SQ SEQUENCE 442 AA; 47172 MW; 22296830 CRC32;

Query Match 4.5%; Score 108.5; DB 1; Length 442;
 Best Local Similarity 21.6%; Pred. No. 0.37;
 Matches 74; Conservative 42; Mismatches 119; Indels 107; Gaps 16;

QY 131 RKILETIFILFAFYQYHT-----YILPSAILM-----GVAAQQLGWLI 170
 DB 10 RYVLGAMLAFLVGVGAQAQTETTSIAEVYAINNLLAAVILVFMQAGFAMLEAGLSS 69

QY 171 HEFAHQHQLKRNRYNDIASFYVGNFLOGRSS-----GGWKEQHNVHHAATN 216
 DB 70 HKNTVNVLFKNTF--DVCVGLLYFLFGSLAYGENPVLGGFFGWSGFGITNNL-----DN 123
 QY 217 VVGRDGDLDLVPYATVAEHLNNYSQDSVMTLFRQHVHVTMLPRLSLWSLQSLIEFV 276
 DB 124 VEGLSPOVD-----WLFQAAFAATAAIVSAGVM 152
 QY 277 SOMPTHYDYRNTAIYEQV-----GLSLHAWSLGQLYFLPDWSTRIMFF-----LVS 325
 DB 153 GRM-----YFKAYLIYSAVITGLVYPISGHMKWGG-----WLDKLGDFHDFAGSLIV 199
 QY 326 HLVGGLLSHVYTFNHYSEKFPALSSNIMSNYACIQIMTRNMRPGRFIDWL-WGGLNYQ 384
 DB 200 HSYGSGFAALAAVVMGPRIGRF--EGNKINSLG-YOGITSSSL--GVFILWGVGYGNP 254
 QY 385 IEHHLFPTPRHNLNLTPLVKE---FAAANGLPYVVDYET 423
 DB 255 SQLAFVGL-----NTNTMLIAVNTTLSAAGGLAALAFDWIT 293

RESULT 13
 FD6C SOYBN STANDARD; PRT; 424 AA.
 ID FD6C SOYBN
 AC P48328;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
 OC Glycine.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SEED;
 RX MEDLINE; 94345008.
 RA HITZ W.D., CARLSON T.J., BOOTH J.R. JR., KINNEY A.J., STECCA K.L.,
 RA YADAV N.S.;
 RT "Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA
 RT and its expression in a cyanobacterium.";
 RL Plant Physiol. 105:635-641(1994).
 CC -!- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -!- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -!- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -!- SIMILARITY: TO OTHER PLANT CHLOROPLAST OMEGA-6 FATTY ACID
 CC DESATURASES.
 CC
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 CC
 CC EMBL; L29215; AAA50158.1;
 DR PFAM; PF00487; FA_desaturase; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KW Transit peptide.
 FT TRANSIT 1 63 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 64 424 OMEGA-6 FATTY ACID DESATURASE.
 FT DOMAIN 165 169 HISTIDINE BOX 1.
 FT DOMAIN 201 205 HISTIDINE BOX 2.
 FT DOMAIN 361 365 HISTIDINE BOX 3.
 SQ SEQUENCE 424 AA; 49641 MW; 6A724470 CRC32;

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OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Caryophyllales; Caryophyllaceae;
OC Spinacia.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-78.
RC STRAIN=CV. SUBITO; TISSUE=LEAF;
RX MEDLINE: 95036044.
RA SCHMIDT H., DRESSLERHAUS T., BUCK F., HEINZ E.;
RT "Purification and PCR-based cDNA cloning of a plastidial n-6
RL Plant Mol. Biol. 26:631-642(1994).
CC -|- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -|- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -|- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -|- SIMILARITY: TO OTHER PLANT CHLOROPLAST OMEGA-6 FATTY ACID
CC DESATURASES.
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CC
CC EMBL: X78311; CAAS5121.1; -.
DR PFAM: PF00487; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transit peptide.
FT CHAIN 1 65 CHLOROPLAST.
FT TRANSIT 66 447 OMEGA-6 FATTY ACID DESATURASE.
FT DOMAIN 171 175 HISTIDINE BOX 1.
FT DOMAIN 207 211 HISTIDINE BOX 2.
FT DOMAIN 367 371 HISTIDINE BOX 3.
SQ SEQUENCE 447 AA; 51306 MW; 7C569B1E CRC32;
Query Match 4.9%; Score 119.5; DB 1; Length 447;
Best Local Similarity 21.8%; Pred. No. 0.056;
Matches 71; Conservative 38; Mismatches 113; Indels 103; Gaps 15;
QY 124 GSPLEFVIRKILETIFILFAFYLYQHYLYPLSAILMGVAQQLGWLII-----HEFAHH 176
DB 128 GTVLISVTSVALGIFIAKAPV-----YLLP-----LAWWTGTAITGFFVIGHDCAHK 176
QY 177 QLFKNRYNDLASYFVGNEL---QGSSGGWKEQHNHVAATNVVGRD-----GDLD 225
DB 177 SFSKNLVEDI-----VCTLAFLPIIYPYEPWRFKDQHTKTNMLREDTAWLPIMKEDIE 232
QY 226 LVP-----FYATVAEHLNNYSQDSWNTLFRQHVHTF-----MLP 262
DB 233 SSPGLRKALIYA-----YGLRTWMSIAHLKLVHFNELKDFRQSEVKRATISLAAVFA 284
QY 263 FLRLSLQSLIFVSQMPHYDYRYNTAIYEQGLSLHAWSLGQLYFLPDKSTRIMEF 322
DB 285 FMVIGMPL---II-----KTGI---VG-----N---IKFW 306
QY 323 LVSHLVGGFLSHVWTFNHYSVKEKFLSSNIMSYACLOIQTMTNRMPRGFIQWLMGGLN 382
DB 307 LMPWLGYHFWS--TFTIVHTATPHIPKSKKWNAAQSLSGIVCHCDYPRWIELCHDIS 365
QY 383 YQIEHLLFTPTMPRHNLNTVNLVKE 407
DB 366 VHIPHISPKIPSYNLRANQSLNE 390
RESULT 11
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CR70_BACTO STANDARD; PRT; 659 AA.
ID CR70_BACTO
AC F17989;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE 75 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN).
GN CRYIIIB.
OS Bacillus thuringiensis (subsp. tolworthi).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=43F;
RX MEDLINE: 90206811.
RA SICK A., GAERTNER F.H., WONG A.;
RT "Nucleotide sequence of a coleopteran-active toxin gene from a new
RT isolate of Bacillus thuringiensis subsp. tolworthi.";
RL Nucleic Acids Res. 18:1305-1305(1990).
CC -|- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -|- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -|- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -|- SIMILARITY: 69% IDENTITY TO THE 70 KD CRYSTAL PROTEIN OF STRAIN
CC TENEBRIONIS (AC P07130).
CC
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CC
CC EMBL: X17123; CAA34983.1; -.
DR EMBL: A07234; CAA00645.1; -.
DR PIR: S10228; S10228.
DR HSSP: P07130; 1DLC.
DR PFAM: PF00355; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 659 AA; 75159 MW; 218F75C3 CRC32;
Query Match 4.6%; Score 111; DB 1; Length 659;
Best Local Similarity 20.7%; Pred. No. 0.38;
Matches 95; Conservative 49; Mismatches 185; Indels 130; Gaps 19;
QY 81 DDPKIGIDDVNMGTNISEKRSA-QINKSFTDLRMVRAEGLMDGSPFYIRKILETIFT 139
DB 150 EDVYNALDSKKAPVNLRSRRSQDRITRELSQAESHFR-----NSMPSFAVSK-FEVLFL 203
QY 140 ILFAFYLYQHYTYPLPSAILMGVAQQLGWLIIHEFAHQLFKNRYND--LASYPVG-NFL 196
DB 204 PTYAQAANTHLLLLKKAQVEGEWGYSSSEDAIEFYQQLKTOQYDHCNVNMYVGNLSL 263
QY 197 QGSSGGWKEQHNHVAATNVVGRDGLDV---PFVAT-----VAEHLNNYSQDSWVM 247
DB 264 RGSTYDAWKFNFRREMTLTV-----LDLIVLFPFDVRLYKGVKVTELTRDTDFIP 318
QY 248 TLFRRQHVHTFMFLPFLRLSWLLQSIIFVSQMPHYDYRYNTAIYEQV--GLS-----L 300
DB 319 TLNALQYEGPTF-----SSSINSIRKPHLFDYLRGIEFHLRPLPGYSGKDSFN 366
QY 301 HWANSL-----GOLYFLPDWSTRIMFLVSHLV 328
DB 367 YWSGNTVETRPSIGSNDTITSPFYGDKSIEPIQKLSFDGQKVYRTIANTDIAAFPDKIY 426
QY 329 GGFLLSHVTVFNHYSVEKFKALSSNIMS----- 356
DB 427 FGVT---KVDFSQDDOKNETSTQTYDSKRYNGYLGQAQSDIDQLPETTDEPLEKAYSHQ 483
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[illegible]

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Db 143 ---PWRKEEYQAGKFMQVT-----YDLFRGAWW--IGSILWA----- 178
Qy 308 QLYFLPDWS-----TRIM-----FFLVSHLVGGFL 332
Db 178 SIHF--DWTKEGKQKQVKESSLLVIGAAIAFTPTMLTIGVWGFKWIPWLVFEW 235
Qy 333 LSHVTFNHYSEKALSNINSVACIQIMTRNRPGRFDWLGGLNYQIEHHLFT 392
Db 236 MS-TFTLLHTIADIPFREPEQWHEASQSGTVHCNYSRWGEFLCHDINVHPHVTTA 294
Qy 393 MPRHNLNTVMPVKE 407
Db 295 IPWYNLRTPTPVYRK 309

RESULT 7
FD6C_ARATH STANDARD; PRT; 418 AA.
AC P46312;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD6 OR FADC.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eumhyllophytes; Spermatophyta; Magnoliophyta; Eudicotyledons;
OC core eudicots; Rosidae; eutosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE; 95148736.
RA FALCONE D.L., GIBSON S., LEMIEUX B., SOMERVILLE C.R.;
RT "Identification of a gene that complements an Arabidopsis mutant
RT deficient in chloroplast omega 6 desaturase activity.";
RL Plant Physiol. 106:1453-1459(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS FOUND IN EXPANDING LEAVES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT CHLOROPLAST OMEGA-6 FATTY ACID
CC DESATURASES.
CC
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CC
CC EMBL; U09503; AAA92800.1;
CC PFAM; PF00487; FA_desaturase; 1.
CC Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
CC Transit peptide.
CC TRANSIT 1 69 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 70 418 OMEGA-6 FATTY ACID DESATURASE.
CC DOMAIN 171 175 HISTIDINE BOX 1.
CC DOMAIN 207 211 HISTIDINE BOX 2.
CC DOMAIN 367 371 HISTIDINE BOX 3.
CC SEQUENCE 418 AA; 47729 MW; C4700789 CRC32;

Query Match 5.1%; Score 125; DB 1; Length 418;
Best Local Similarity 21.7%; Pred. No. 0.02;

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Matches 73; Conservative 47; Mismatches 132; Indels 84; Gaps 14;
Qy 111 DLRMVRVREGLMDGSP--LFYI--RKILETIFLFAFYLOYHTYVLPSPAILMGVAWQOL 166
Db 100 DLPENVTLKDINDTPKEVFEIDDLKALKSVLSVTSYTLGLPMIAKSPWLLPLAWMT 159
Qy 167 GWLI-----HEFAHQFLFKNRYNDLASIFYGN--FLQ-GFSSGGKWKQHNHVAATN 216
Db 160 GTAITGFFVIGHDCAKHSKKNLVEDI---VGTIAFLPLVYPYEPWREKDRHAKTN 215
Qy 217 VVGRDGLDLVP---FYATVAEH---LNNYSQDSWVMTLFRWQHVVHVTML----- 262
Db 216 MLVHDTAWQVPPEEPESPVMRKAIIFGYGPIRPWLSIAHW--VNMHFNKKFRASEVN 273
Qy 262 -----PELRLSWLLQSIIFVSQMPHYDYRNATYIYEQVGLSLHWANSLGOLYF 311
Db 274 RVKISLACVFAFMAVGWPL-----IVYKGI-LGM----- 303
Qy 312 LPDWSIRIMFFVLSHLVGGFLSHVVTENHYSEKALSNINSVACIQIMTRNMRPG 371
Db 303 -----VKFWLMPWLGCFHWMS-TFTMVHTAPHIPFRPADEWNAQAOLNGTVHCDYP 354
Qy 372 RFIDWLGGLNYQIEHHLFTPTMPRNLNTVMPVKE 407
Db 355 SWIEILCHDINVPHHISPRIPSYNLRAAHSIQE 390

RESULT 8
DESA_SYNY3
ID DESA_SYNY3 STANDARD; PRT; 351 AA.
AC P20388;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE FATTY ACID DESATURASE (EC 1.14.99.-) (DELTA 12 DESATURASE).
GN DESA OR SLR1350.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90370121.
RA WADA H., GOMBOS Z., MURATA N.;
RT "Enhancement of chilling tolerance of a cyanobacterium by genetic
RT manipulation of fatty acid desaturation.";
RL Nature 347:200-203(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,
RA OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,
RA YAMADA M., YASUDA M., TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
CC POSITION OF FATTY ACID BOUND TO MEMBRANE GLYCEROLIPIDS. THIS
CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON
CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.
CC -1- SIMILARITY: TO PLANTS STEAROYL-ACP DESATURASE.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X53508; CAA37584.1;
CC
CC

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CC DNA are used as probes to isolate related coding sequences. Recombinant plants can produce high yields of PUFA, since new pathways can be created and unwanted ones suppressed. Plants can be engineered to express oils of particular PUFA composition, e.g. One similar to that in human milk, and product recovery is simpler than with e.g. fish.

CC Sequence 457 AA:

CC 124 GSPFYIRKI-----LETIFTILFAFYLOHYTY-YLPSSAILMGVAQOGLWLIHFAHQ 177

CC 119 SSKAYAFKVSFNLCITWGLSTVIVAKGQSTLANVLSAALLGLFWQCGWLAHDFLHQ 178

CC 178 LFKNRYNDLASFYFVGNFLQGFSSGGKQKHNVHHAATNVVGRDGLDLPVFAVAEHL 237

CC 179 VFQDRFWGLDFAFLGCVGCGFSSSSWKKHNTTHAHPNVHGEDPDDIDHPL-LTWSEHA 237

CC 238 NNYSD-----SWYMTLFRQVHWTFF--MLPFLRLSWLLQSIIFV-----SQ 278

CC 238 LEWSDVPDEELTRMWSREMLNQTWFFPILSFARLSWCLQSIILVLPNGOAHKPSGAR 297

CC 279 MPTHYDIYRNTAIVQVGLSHWASLGOLY-FLPDWSTRIMFFLVSHLVGFLLSHVY 337

CC 298 VP-----ISLVEQLSLAMHWTYLATMELFIKDPVNMVLYFLVSAVCGNLLAIVF 348

CC 338 TFNHSYVERKALSSNMSNVACLOIMTTRNMRPGRIDWLGGLNLYQIEHHLPPTMPRIN 397

CC 349 SLNHGMPVISKEEAVDMDFFTKIITGRDVHPGLFANWFTGGLNLYQIEHHLPPTMPRIN 408

CC 398 LNTVMPLKEFAAANGPLVMYDDYFTGFWLEIEQFNRNIANAAKLT 444

CC 409 FSKIOPAVETLCKKYNRYHTTGMIETAEVFSRLNEVSKAASKMGK 455

CC W95504 standard; peptide: 457 AA.

CC AC W95504:

CC DE 26-MAR-1999 (first entry)

CC DE Mortierella alpina delta 6 desaturase.

CC KW Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil; polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic; stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula; dietary supplement; prostaglandin; restenosis; angioplasty; inflammation; rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS; diabetes; cosmetic; animal feed.

CC OS Mortierella alpina.

CC PN W09846764-A1.

CC PD 22-OCT-1998.

CC PF 10-APR-1998; U07421.

CC PR 24-OCT-1997; US-956985.

CC PR 11-APR-1997; US-833610.

CC PR 11-APR-1997; US-834033.

CC PR 11-APR-1997; US-834655.

CC PA (ABBO) ABBOTT LAB.

CC PA (CALJ) CALGENE LLC.

CC PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P, Thurmond J.

CC PI WPI: 99-080739/07.

CC DR N-PSDB: X00889.

CC DR Nucleic acid construct able to express fatty acid desaturase in plants - useful in human or animal nutrition, as cosmetics and therapeutically, e.g. for restenosis, cancer and diabetes

CC PT Claim 7; Fig 3A-E; 210pp; English.

CC PS This represents a Mortierella alpina delta 6 desaturase. The invention relates to a nucleic acid construct that contains at least one of the nucleotide sequences (X00889 to X00891) encoding M. alpina delta 6, delta 12 and delta 5 desaturases (W95504 to W95506) respectively, coupled to an expression control sequence functional in plants. Recombinant plant cells containing at least one DNA encoding a M. alpina fatty acid desaturase (FAD), can be used for the production of polyunsaturated fatty acid (PUFA). These recombinant cells or plants containing them are used to produce oils such as linoleic acid, arachidonic acid, gamma-linolenic acid, dihomogamma-linolenic acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are used: (i) to treat malnutrition; (ii) in infant feeding formulas; or dietary supplements or substitutes, for use in humans or animals; (iii) for treating disorders associated with inadequate consumption or production of PUFA (or their metabolites such as prostaglandins), e.g. restenosis after angioplasty, inflammation, CC AIDS, rheumatoid arthritis, psoriasis, osteoporosis, cancer, eczema, CC diabetes; (iv) as cosmetics, and (v) as animal feeds. Fragments of the

CC Query Match 25.8%; Score 629; DB 1; Length 457;

CC Best Local Similarity 33.0%; Pred. No. 1.2e-56;

CC Matches 154; Conservative 76; Mismatches 175; Indels 62; Gaps 13;

CC QY 4 RQEEHEPFPIKIDGKWCQIDDAVLRSHPGSGSALTITKYNMDATVFTFTGSKAEQWLT 63

CC DB 25 KDAEAPFLMIDNKVDVRETV-PDHGSGSVILHVGKDGTDVDFTFH---PEA-AWET 79

CC QY 64 ELKCEPTQEPPIKIDDPKIGDIDVNMGTNISEKRSQAQNKSTDLRMVRVRAEGLMD 123

CC DB 80 LANFYVGDIDESDRDKNDDF-----AAEVRK-----LRTLFSGLGYD 118

CC QY 124 GSPFYIRKI-----LETIFTILFAFYLOHYTY-YLPSSAILMGVAQOGLWLIHFAHQ 177

CC DB 119 SSKAYAFKVSFNLCITWGLSTVIVAKGQSTLANVLSAALLGLFWQCGWLAHDFLHQ 178

CC QY 178 LFKNRYNDLASFYFVGNFLQGFSSGGKQKHNVHHAATNVVGRDGLDLPVFAVAEHL 237

CC DB 179 VFQDRFWGLDFAFLGCVGCGFSSSSWKKHNTTHAHPNVHGEDPDDIDHPL-LTWSEHA 237

CC QY 238 NNYSD-----SWYMTLFRQVHWTFF--MLPFLRLSWLLQSIIFV-----SQ 278

CC DB 238 LEWSDVPDEELTRMWSREMLNQTWFFPILSFARLSWCLQSIILVLPNGOAHKPSGAR 297

CC QY 279 MPTHYDIYRNTAIVQVGLSHWASLGOLY-FLPDWSTRIMFFLVSHLVGFLLSHVY 337

CC DB 298 VP-----ISLVEQLSLAMHWTYLATMELFIKDPVNMVLYFLVSAVCGNLLAIVF 348

CC QY 338 TFNHSYVERKALSSNMSNVACLOIMTTRNMRPGRIDWLGGLNLYQIEHHLPPTMPRIN 397

CC DB 349 SLNHGMPVISKEEAVDMDFFTKIITGRDVHPGLFANWFTGGLNLYQIEHHLPPTMPRIN 408

CC QY 398 LNTVMPLKEFAAANGPLVMYDDYFTGFWLEIEQFNRNIANAAKLT 444

CC DB 409 FSKIOPAVETLCKKYNRYHTTGMIETAEVFSRLNEVSKAASKMGK 455

CC RESULT 3

CC W85121

CC ID W85121 standard; Protein: 457 AA.

CC DE 11-FEB-1999 (first entry)

CC KW A delta-6 desaturase enzyme amino acid sequence.

CC KW Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder.

CC OS Unidentified.

CC PN W09846765-A1.

CC PD 22-OCT-1998.

CC PF 10-APR-1998; U07422.

CC PR 11-APR-1997; US-833610.

CC PA (ABBO) ABBOTT LAB.

CC PA (CALJ) CALGENE LLC.

CC PI Chaudhary S, Huang Y, Knutson D, Leonard AE, Mukerji P, Thurmond J.

CC PI WPI: 99-009334/01.

CC DR New nucleic acid encoding delta5 and other desaturase enzymes - useful in production of oils of increased arachidonic acid content, used, e.g. for treating cancer, as foods, animal feeds and cosmetics

CC PS Disclosure: Pages 95-96; 153pp; English.

CC The present sequence represents a fatty acid delta-6 desaturase enzyme.

CC The specification describes methods for desaturating a fatty acid and

Q920R9
ID Q920R9 PRELIMINARY; PRT; 444 AA.
AC Q920R9;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95085046.
RA CHO H.P., NAKAMURA M.T., CLARKE S.D.;
RT "Cloning, expression, and nutritional regulation of the mammalian
Delta-6 desaturase."
RL J. Biol. Chem. 274:471-477(1999).
DR EMBL; AF126798; AAD20017.1; -
DR HSSP; P00171; 3B5C.
SQ SEQUENCE 444 AA; 52387 MW; F6F9668B CRC32;

Query Match 18.9%; Score 432; DB 11; Length 444;
Best Local Similarity 28.1%; Pred. No. 4.3e-32;
Matches 121; Conservative 67; Mismatches 182; Indels 60; Gaps 12;
Qy 3 SKRQALSP-----LQMEQTYDVSANVNFHFGGAEIENYQGRDATDA 45
Db 12 TERQAPMPFWEIEIQHNLRDRLVLDKRVYNTKWSQRHGGHVRVGHYSGEDATDA 71
Qy 46 ENVMH---FQAEFDKLRMPKINPSFELPPQAAVNEAQEDFKRLREELIATCMEDASPL 101
Db 72 FRAHLDLDFVKFLAPLIGELAPEPSLDKSKSQTEDFFRALAKRTAEDMNLFTNHL 131
Qy 102 WYSKISTTLGLGVLYFLMVQYQMYF-----ICAVLLGMHYQMGWLSHDICHQHT 153
Db 132 FFFELLSHIIVMESLAWFIL---SYFGTGWIPLTATFVLATVSAQAGWLQHDYGLSV 187
Qy 154 FNRNKNVNLVGLFNGLOGFSVTCWKDRHNAHSATNVQGHDPDINDLPLAWSDDVT 213
Db 188 YKKSINWVYVHRFVIGHLKGASANWNNRHFQHHAKPNIFHKDPDKSLHVFVLGEWQPL 247
Qy 214 RASPSIRKLQF---QOYFLV-ICILLRFNCFQCVLTVRSUKDRDNQFYRSQYKKEAI 269
Db 248 EYKKKLKLVPYNHQHEYFELGPPLLIIPWFOYQIIMTISRDR----- 293
Qy 270 GLAHLHTLALFHLF--FMP--SILTSLLVFFVSELVGGFGIAIVVFMNHYPLEKIDPV 325
Db 293 WDLAWAISYVMREFYTIIPFYIGLALVFLNFIRLESHWFWVVTQMNLVMEIDLHY 352
Qy 326 WDGHGFSVQIHTNMNIRGIITDWFGLNTOIEHHLWPTLPRHNLTAVSQVQVEOLCOK 395
Db 353 RD--WFS--SOLAATCNVEQSFNDWFSGLHNFQIEHHLFPTPRHNLKIAPLVKSILCAK 409
Qy 386 HNLVYR-NPL 394
Db 410 HGIEIQERPL 419

RESULT 14
Q92TU8
ID Q92TU8 PRELIMINARY; PRT; 469 AA.
AC Q92TU8;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE S276.
GN S276.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euryhallophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Triticum.
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-CV, ET3;
RA DELRAIZE E., HEBB D.M., GARDNER R.C., RICHARDS K.D.;
RT "Aluminum tolerance in yeast conferred by over-expression of wheat
genes."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031194; AAD10250.1; -
DR HSSP; P00171; 3B5C.
DR MENDEL; 35849; Triale; 2419; 35849.
SQ SEQUENCE 469 AA; 52617 MW; E52DB451 CRC32;

Query Match 18.8%; Score 430; DB 10; Length 469;
Best Local Similarity 27.4%; Pred. No. 7.2e-32;
Matches 126; Conservative 68; Mismatches 168; Indels 98; Gaps 15;
Qy 11 LQMEQTYDVSANVNFHFGGAEIENYQGRDATDAFVMVHFOEAFDKLRMPKINP--- 67
Db 46 ISISGDVYDVTPLRHRHPGGEVPLITLAGODATDAFMAVH-----PPSVRPLLR 95
Qy 67 -----SPELPQAAVNEAQEDFKRLREELIATMGFDASPLWYSKISTTLGLGVLYGF 119
Db 96 FVGRLTDTYVPPASA-----DFRRLAQLSSAGLFR-----VGHTPKF 135
Qy 120 LMVQYQMYFIGAV-----LLGMHYQMGWLSHDICHQHTFKNRNNNL 162
Db 136 LLVAMSVLFCIALYCVLACSTGAHMFAGGLIGFIQSGWIGHDSGHQHTIRHPALNRL 195
Qy 163 VGLVFGNGQGGFSVTCWKDRHNAHSATNVQGHDPDINDLPLA-----WS--EDD 211
Db 196 LQVVSNCITGLGIAWKNHNTHHSCNSLDHDPDLQHLPLFAVSTKFNENLWSVCYER 255
Qy 212 VTRASPSIRKLQFQOYFELVICILLRFNCFQCV---LTVRSUKDRDNQFYRSQYKKEA 268
Db 256 TLAFDAISFFSVYQHWTEFVPMGFARINLLVQSIVELITQKKVRQ-----WLEI 306
Qy 269 IGLAHLHTLALFHLFMPFSILTSLLVFF--VSELVGGF--GIAIVWF-MNHY-PLEKI 321
Db 307 AGVAAEFV-----WYPLLVSCLPNMWERVAFLASVITGIQHVQFCNLHFSSAVYV 358
Qy 322 GPPVMDGHGFSVQIHTNMNIRGIITDWFGLNTOIEHHLWPTLPRHNLTAVSQVQVEQ 381
Db 359 GPP--KGNDWFERQTAGTLDIKSPWMDWFGHGLQFQVEHHLFPLPRCHRYMVAPIVRD 416
Qy 382 LQCKHNLPRNPLPHEGLVILLRYLAVFARMAEKQAPAGKA 421
Db 417 LCKKHGLSYGAATFEANVTMTKTLRAAALQAREATTGAA 456

RESULT 15
Q92122
ID Q92122 PRELIMINARY; PRT; 444 AA.
AC Q92122;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE DAWLEY; TISSUE-LIVER;
RA AKI T., SHIMADA Y., INAGAKI K., HIGASHIMOTO H., KAWAMOTO S.,
RA SHIGETA S., ONO K., SUZUKI O.;
RT "Molecular cloning and functional characterization of rat delta-6
fatty acid desaturase."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021980; BAA75496.1; -
DR HSSP; P00171; 3B5C.
SQ SEQUENCE 444 AA; 52380 MW; A5E5B487 CRC32;

Search completed: February 25, 2000, 02:55:31
Job time: 17534 sec